

<110> Martin Richard  
Flatt Brenton Todd  
Kahl Jeffrey Dean  
Wang Tie-Lin

<130> 38205-3001B

<150> 10/329.668

<151> 2002-12-20

<150> 60/342.720

<151> 2001-12-21

<160> 18

<170> FastSEQ for Windows Version 4.0

 $\langle 210 \rangle$  1

<211> 1528

<212> DNA

<213> Homo Sapien

 $\langle 220 \rangle$ 

<221> CDS

 $\langle 222 \rangle \quad (36) \dots (1379)$ 

<300>

<308> GeneBank Nm 005693

<309> 2002-05-14

<400> 1

cagtgccttg gtaatgacca gggctccaga aagag atg tcc ttg tgg ctg ggg 53  
Met Ser Leu Trp Leu Gly  
1 5

gcc cct gtg cct gac att cct cct gac tct gcg gtg gag ctg tgg aag 101  
Ala Pro Val Pro Asp Ile Pro Pro Asp Ser Ala Val Glu Leu Trp Lys  
10 15 20

cca ggc gca cag gat gca agc agc cag gcc cag gga ggc agc agc tgc 149  
Pro Gly Ala Gln Asp Ala Ser Ser Gln Ala Gln Gly Gly Ser Ser Cys  
25 30 35

atc ctc aga gag gaa gcc agg atg ccc cac tct gct ggg ggt act gca 197  
Ile Leu Arg Glu Glu Ala Arg Met Pro His Ser Ala Gly Gly Thr Ala  
40 45 50

ggg gtg ggg ctg gag gct gca gag ccc aca gcc ctg ctc acc agg gca 245  
Gly Val Gly Leu Glu Ala Ala Glu Pro Thr Ala Leu Leu Thr Arg Ala  
55 60 65 70

gag ccc cct tca gaa ccc aca gag atc cgt cca caa aag cgg aaa aag 293  
Glu Pro Pro Ser Glu Pro Thr Glu Ile Arg Pro Gln Lys Arg Lys Lys  
75 80 85

ggg cca gcc ccc aaa atg ctg ggg aac gag cta tgc agc gtg tgt ggg 341  
Gly Pro Ala Pro Lys Met Leu Gly Asn Glu Leu Cys Ser Val Cys Gly

90										95					100					
gac	aag	gcc	tcg	ggc	ttc	cac	tac	aat	gtt	ctg	agc	tgc	gag	ggc	tgc	389				
Asp	Lys	Ala	Ser	Gly	Phe	His	Tyr	Asn	Val	Leu	Ser	Cys	Glu	Gly	Cys					
		105					110					115								
aag	gga	ttc	ttc	cgc	cgc	agc	gtc	atc	aag	gga	gcg	cac	tac	atc	tgc	437				
Lys	Gly	Phe	Phe	Arg	Arg	Ser	Val	Ile	Lys	Gly	Ala	His	Tyr	Ile	Cys					
	120					125					130									
cac	agt	ggc	ggc	cac	tgc	ccc	atg	gac	acc	tac	atg	cgt	cgc	aag	tgc	485				
His	Ser	Gly	Gly	His	Cys	Pro	Met	Asp	Thr	Tyr	Met	Arg	Arg	Lys	Cys					
135					140					145					150					
cag	gag	tgt	cgg	ctt	cgc	aaa	tgc	cgt	cag	gct	ggc	atg	cgg	gag	gag	533				
Gln	Glu	Cys	Arg	Leu	Arg	Lys	Cys	Arg	Gln	Ala	Gly	Met	Arg	Glu	Glu					
				155					160					165						
tgt	gtc	ctg	tca	gaa	gaa	cag	atc	cgc	ctg	aag	aaa	ctg	aag	cgg	caa	581				
Cys	Val	Leu	Ser	Glu	Glu	Gln	Ile	Arg	Leu	Lys	Lys	Leu	Lys	Arg	Gln					
			170					175					180							
gag	gag	gaa	cag	gct	cat	gcc	aca	tcc	ttg	ccc	ccc	agg	cgt	tcc	tca	629				
Glu	Glu	Glu	Gln	Ala	His	Ala	Thr	Ser	Leu	Pro	Pro	Arg	Arg	Ser	Ser					
		185					190					195								
ccc	ccc	caa	atc	ctg	ccc	cag	ctc	agc	ccg	gaa	caa	ctg	ggc	atg	atc	677				
Pro	Pro	Gln	Ile	Leu	Pro	Gln	Leu	Ser	Pro	Glu	Gln	Leu	Gly	Met	Ile					
	200					205					210									
gag	aag	ctc	gtc	gct	gcc	cag	caa	cag	tgt	aac	cgg	cgc	tcc	ttt	tct	725				
Glu	Lys	Leu	Val	Ala	Ala	Gln	Gln	Gln	Cys	Asn	Arg	Arg	Ser	Phe	Ser					
215					220				225						230					
gac	cgg	ctt	cga	gtc	acg	cct	tgg	ccc	atg	gca	cca	gat	ccc	cat	agc	773				
Asp	Arg	Leu	Arg	Val	Thr	Pro	Trp	Pro	Met	Ala	Pro	Asp	Pro	His	Ser					
				235				240						245						
cgg	gag	gcc	cgt	cag	cag	cgc	ttt	gcc	cac	ttc	act	gag	ctg	gcc	atc	821				
Arg	Glu	Ala	Arg	Gln	Gln	Arg	Phe	Ala	His	Phe	Thr	Glu	Leu	Ala	Ile					
			250					255					260							
gtc	tct	gtg	cag	gag	ata	gtt	gac	ttt	gct	aaa	cag	cta	ccc	ggc	ttc	869				
Val	Ser	Val	Gln	Glu	Ile	Val	Asp	Phe	Ala	Lys	Gln	Leu	Pro	Gly	Phe					
		265					270					275								
ctg	cag	ctc	agc	cgg	gag	gac	cag	att	gcc	ctg	ctg	aag	acc	tct	gcg	917				
Leu	Gln	Leu	Ser	Arg	Glu	Asp	Gln	Ile	Ala	Leu	Leu	Lys	Thr	Ser	Ala					
	280					285					290									
atc	gag	gtg	atg	ctt	ctg	gag	aca	tct	cgg	agg	tac	aac	cct	ggg	agt	965				
Ile	Glu	Val	Met	Leu	Leu	Glu	Thr	Ser	Arg	Arg	Tyr	Asn	Pro	Gly	Ser					
295					300				305						310					
gag	agt	atc	acc	ttc	ctc	aag	gat	ttc	agt	tat	aac	cgg	gaa	gac	ttt	1013				
Glu	Ser	Ile	Thr	Phe	Leu	Lys	Asp	Phe	Ser	Tyr	Asn	Arg	Glu	Asp	Phe					
				315				320						325						
gcc	aaa	gca	ggg	ctg	caa	gtg	gaa	ttc	atc	aac	ccc	atc	ttc	gag	ttc	1061				
Ala	Lys	Ala	Gly	Leu	Gln	Val	Glu	Phe	Ile	Asn	Pro	Ile	Phe	Glu	Phe					
			330					335					340							
tcc	agg	gcc	atg	aat	gag	ctg	caa	ctc	aat	gat	gcc	gag	ttt	gcc	ttg	1109				
Ser	Arg	Ala	Met	Asn	Glu	Leu	Gln	Leu	Asn	Asp	Ala	Glu	Phe	Ala	Leu					
		345					350					355								
ctc	att	gct	atc	agc	atc	ttc	tct	gca	gac	cgg	ccc	aac	gtg	cag	gac	1157				

```

Leu Ile Ala Ile Ser Ile Phe Ser Ala Asp Arg Pro Asn Val Gln Asp
 360                               365                               370

cag ctc cag gtg gag agg ctg cag cac aca tat gtg gaa gcc ctg cat 1205
Gln Leu Gln Val Glu Arg Leu Gln His Thr Tyr Val Glu Ala Leu His
375                               380                               385                               390

gcc tac gtc tcc atc cac cat ccc cat gac cga ctg atg ttc cca cgg 1253
Ala Tyr Val Ser Ile His His Pro His Asp Arg Leu Met Phe Pro Arg
                               395                               400                               405

atg cta atg aaa ctg gtg agc ctc cgg acc ctg agc agc gtc cac tca 1301
Met Leu Met Lys Leu Val Ser Leu Arg Thr Leu Ser Ser Val His Ser
                               410                               415                               420

gag caa gtg ttt gca ctg cgt ctg cag gac aaa aag ctc cca ccg ctg 1349
Glu Gln Val Phe Ala Leu Arg Leu Gln Asp Lys Lys Leu Pro Pro Leu
                               425                               430                               435

ctc tct gag atc tgg gat gtg cac gaa tga ctgttctgtc cccatatttt 1399
Leu Ser Glu Ile Trp Asp Val His Glu *
                               440                               445

ctgtttttctt ggccggatgg ctgaggcctg gtggctgcct cctagaagtg gaacagactg 1459
agaagggcaa acattcctgg gagctgggca aggagatcct cccgtggcat taaaagagag 1519
tcaaagggt 1528

```

```

<210> 2
<211> 447
<212> PRT
<213> Homo Sapien

```

```

<400> 2
Met Ser Leu Trp Leu Gly Ala Pro Val Pro Asp Ile Pro Pro Asp Ser
 1                               5                               10                               15
Ala Val Glu Leu Trp Lys Pro Gly Ala Gln Asp Ala Ser Ser Gln Ala
                               20                               25                               30
Gln Gly Gly Ser Ser Cys Ile Leu Arg Glu Glu Ala Arg Met Pro His
                               35                               40                               45
Ser Ala Gly Gly Thr Ala Gly Val Gly Leu Glu Ala Ala Glu Pro Thr
                               50                               55                               60
Ala Leu Leu Thr Arg Ala Glu Pro Pro Ser Glu Pro Thr Glu Ile Arg
65                               70                               75                               80
Pro Gln Lys Arg Lys Lys Gly Pro Ala Pro Lys Met Leu Gly Asn Glu
                               85                               90                               95
Leu Cys Ser Val Cys Gly Asp Lys Ala Ser Gly Phe His Tyr Asn Val
                               100                               105                               110
Leu Ser Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Ile Lys
                               115                               120                               125
Gly Ala His Tyr Ile Cys His Ser Gly Gly His Cys Pro Met Asp Thr
                               130                               135                               140
Tyr Met Arg Arg Lys Cys Gln Glu Cys Arg Leu Arg Lys Cys Arg Gln
145                               150                               155                               160
Ala Gly Met Arg Glu Glu Cys Val Leu Ser Glu Glu Gln Ile Arg Leu
                               165                               170                               175
Lys Lys Leu Lys Arg Gln Glu Glu Glu Gln Ala His Ala Thr Ser Leu
                               180                               185                               190
Pro Pro Arg Arg Ser Ser Pro Pro Gln Ile Leu Pro Gln Leu Ser Pro
                               195                               200                               205
Glu Gln Leu Gly Met Ile Glu Lys Leu Val Ala Ala Gln Gln Gln Cys
                               210                               215                               220
Asn Arg Arg Ser Phe Ser Asp Arg Leu Arg Val Thr Pro Trp Pro Met
225                               230                               235                               240
Ala Pro Asp Pro His Ser Arg Glu Ala Arg Gln Gln Arg Phe Ala His
                               245                               250                               255
Phe Thr Glu Leu Ala Ile Val Ser Val Gln Glu Ile Val Asp Phe Ala
                               260                               265                               270

```



His	Tyr	Asn	Val	Leu	Ser	Cys	Glu	Gly	Cys	Lys	Gly	Phe	Phe	Arg	Arg		
		100					105					110					
agt	gtg	gtc	cgt	ggg	ggg	gcc	agg	cgc	tat	gcc	tgc	cgg	ggg	ggc	gga	442	
Ser	Val	Val	Arg	Gly	Gly	Ala	Arg	Arg	Tyr	Ala	Cys	Arg	Gly	Gly	Gly		
	115					120					125						
acc	tgc	cag	atg	gac	gct	ttc	atg	cgg	cgc	aag	tgc	cag	cag	tgc	cgg	490	
Thr	Cys	Gln	Met	Asp	Ala	Phe	Met	Arg	Arg	Lys	Cys	Gln	Gln	Cys	Arg		
130					135					140					145		
ctg	cgc	aag	tgc	aag	gag	gca	ggg	atg	agg	gag	cag	tgc	gtc	ctt	tct	538	
Leu	Arg	Lys	Cys	Lys	Glu	Ala	Gly	Met	Arg	Glu	Gln	Cys	Val	Leu	Ser		
				150					155					160			
gaa	gaa	cag	atc	cgg	aag	aag	aag	att	cgg	aaa	cag	cag	cag	gag	tca	586	
Glu	Glu	Gln	Ile	Arg	Lys	Lys	Lys	Ile	Arg	Lys	Gln	Gln	Gln	Glu	Ser		
			165					170					175				
cag	tca	cag	tcg	cag	tca	cct	gtg	ggg	ccg	cag	ggc	agc	agc	agc	tca	634	
Gln	Ser	Gln	Ser	Gln	Ser	Pro	Val	Gly	Pro	Gln	Gly	Ser	Ser	Ser	Ser		
		180					185					190					
gcc	tct	ggg	cct	ggg	gct	tcc	cct	ggg	gga	tct	gag	gca	ggc	agc	cag	682	
Ala	Ser	Gly	Pro	Gly	Ala	Ser	Pro	Gly	Gly	Ser	Glu	Ala	Gly	Ser	Gln		
	195					200					205						
ggc	tcc	ggg	gaa	ggc	gag	ggg	gtc	cag	cta	aca	gcg	gct	caa	gaa	cta	730	
Gly	Ser	Gly	Glu	Gly	Glu	Gly	Val	Gln	Leu	Thr	Ala	Ala	Gln	Glu	Leu		
210				215						220				225			
atg	atc	cag	cag	ttg	gtg	gcg	gcc	caa	ctg	cag	tgc	aac	aaa	cgc	tcc	778	
Met	Ile	Gln	Gln	Leu	Val	Ala	Ala	Gln	Leu	Gln	Cys	Asn	Lys	Arg	Ser		
				230					235					240			
ttc	tcc	gac	cag	ccc	aaa	gtc	acg	ccc	tgg	ccc	ctg	ggc	gca	gac	ccc	826	
Phe	Ser	Asp	Gln	Pro	Lys	Val	Thr	Pro	Trp	Pro	Leu	Gly	Ala	Asp	Pro		
			245					250					255				
cag	tcc	cga	gat	gcc	cgc	cag	caa	cgc	ttt	gcc	cac	ttc	acg	gag	ctg	874	
Gln	Ser	Arg	Asp	Ala	Arg	Gln	Gln	Arg	Phe	Ala	His	Phe	Thr	Glu	Leu		
		260					265					270					
gcc	atc	atc	tca	gtc	cag	gag	atc	gtg	gac	ttc	gct	aag	caa	gtg	cct	922	
Ala	Ile	Ile	Ser	Val	Gln	Glu	Ile	Val	Asp	Phe	Ala	Lys	Gln	Val	Pro		
	275					280					285						
ggg	ttc	ctg	cag	ctg	ggc	cgg	gag	gac	cag	atc	gcc	ctc	ctg	aag	gca	970	
Gly	Phe	Leu	Gln	Leu	Gly	Arg	Glu	Asp	Gln	Ile	Ala	Leu	Leu	Lys	Ala		
290					295					300					305		
tcc	act	atc	gag	atc	atg	ctg	cta	gag	aca	gcc	agg	cgc	tac	aac	cac	1018	
Ser	Thr	Ile	Glu	Ile	Met	Leu	Leu	Glu	Thr	Ala	Arg	Arg	Tyr	Asn	His		
				310					315					320			
gag	aca	gag	tgt	atc	acc	ttc	ttg	aag	gac	ttc	acc	tac	agc	aag	gac	1066	
Glu	Thr	Glu	Cys	Ile	Thr	Phe	Leu	Lys	Asp	Phe	Thr	Tyr	Ser	Lys	Asp		
			325					330					335				
gac	ttc	cac	cgt	gca	ggc	ctg	cag	gtg	gag	ttc	atc	aac	ccc	atc	ttc	1114	
Asp	Phe	His	Arg	Ala	Gly	Leu	Gln	Val	Glu	Phe	Ile	Asn	Pro	Ile	Phe		
		340				345						350					
gag	ttc	tcg	cgg	gcc	atg	cgg	cgg	ctg	ggc	ctg	gac	gac	gct	gag	tac	1162	
Glu	Phe	Ser	Arg	Ala	Met	Arg	Arg	Leu	Gly	Leu	Asp	Asp	Ala	Glu	Tyr		
	355					360					365						

gcc	ctg	ctc	atc	gcc	atc	aac	atc	ttc	tcg	gcc	gac	cgg	ccc	aac	gtg	1210
Ala	Leu	Leu	Ile	Ala	Ile	Asn	Ile	Phe	Ser	Ala	Asp	Arg	Pro	Asn	Val	
370					375					380					385	
cag	gag	ccg	ggc	cgc	gtg	gag	gcg	ttg	cag	cag	ccc	tac	gtg	gag	gcg	1258
Gln	Glu	Pro	Gly	Arg	Val	Glu	Ala	Leu	Gln	Gln	Pro	Tyr	Val	Glu	Ala	
				390					395					400		
ctg	ctg	tcc	tac	acg	cgc	atc	aag	agg	ccg	cag	gac	cag	ctg	cgc	ttc	1306
Leu	Leu	Ser	Tyr	Thr	Arg	Ile	Lys	Arg	Pro	Gln	Asp	Gln	Leu	Arg	Phe	
			405					410					415			
ccg	cgc	atg	ctc	atg	aag	ctg	gtg	agc	ctg	cgc	acg	ctg	agc	tct	gtg	1354
Pro	Arg	Met	Leu	Met	Lys	Leu	Val	Ser	Leu	Arg	Thr	Leu	Ser	Ser	Val	
		420					425					430				
cac	tcg	gag	cag	gtc	ttc	gcc	ttg	cgg	ctc	cag	gac	aag	aag	ctg	ccg	1402
His	Ser	Glu	Gln	Val	Phe	Ala	Leu	Arg	Leu	Gln	Asp	Lys	Lys	Leu	Pro	
		435				440					445					
cct	ctg	ctg	tcg	gag	atc	tgg	gac	gtc	cac	gag	tga	ggggctggcc				1448
Pro	Leu	Leu	Ser	Glu	Ile	Trp	Asp	Val	His	Glu	*					
450					455					460						

accagcccc	acagccttgc	ctgaccaccc	tccagcagat	agacgccggc	acccttctct	1508
cttcctaggg	tggaggggc	cctgggccga	gcctgtagac	ctatcggctc	tcatcccttg	1568
ggataagccc	cagtccaggt	ccaggaggct	ccctccctgc	ccagcgagtc	ttccagaagg	1628
ggtgaaaggg	ttgcagggtcc	cgaccactga	cccttcccgg	ctgccctccc	tccccagctt	1688
acacctcaag	cccagcacgc	agtgcacctt	gaacagaggg	aggggaggac	ccatggctct	1748
ccccctagc	ccgggagacc	agggccttcc	tcttctctctg	cttttattta	ataaaaaacta	1808
aaaacag						1815

<210> 4  
 <211> 460  
 <212> PRT  
 <213> Homo Sapien

<400> 4																
Met	Ser	Ser	Pro	Thr	Thr	Ser	Ser	Leu	Asp	Thr	Pro	Leu	Pro	Gly	Asn	
1				5					10					15		
Gly	Pro	Pro	Gln	Pro	Gly	Ala	Pro	Ser	Ser	Ser	Pro	Thr	Val	Lys	Glu	
			20					25					30			
Glu	Gly	Pro	Glu	Pro	Trp	Pro	Gly	Gly	Pro	Asp	Pro	Asp	Val	Pro	Gly	
		35					40					45				
Thr	Asp	Glu	Ala	Ser	Ser	Ala	Cys	Ser	Thr	Asp	Trp	Val	Ile	Pro	Asp	
	50					55				60						
Pro	Glu	Glu	Glu	Pro	Glu	Arg	Lys	Arg	Lys	Lys	Gly	Pro	Ala	Pro	Lys	
65				70					75						80	
Met	Leu	Gly	His	Glu	Leu	Cys	Arg	Val	Cys	Gly	Asp	Lys	Ala	Ser	Gly	
			85					90						95		
Phe	His	Tyr	Asn	Val	Leu	Ser	Cys	Glu	Gly	Cys	Lys	Gly	Phe	Phe	Arg	
			100					105					110			
Arg	Ser	Val	Val	Arg	Gly	Gly	Ala	Arg	Arg	Tyr	Ala	Cys	Arg	Gly	Gly	
		115					120					125				
Gly	Thr	Cys	Gln	Met	Asp	Ala	Phe	Met	Arg	Arg	Lys	Cys	Gln	Gln	Cys	
	130					135					140					
Arg	Leu	Arg	Lys	Cys	Lys	Glu	Ala	Gly	Met	Arg	Glu	Gln	Cys	Val	Leu	
145				150					155						160	
Ser	Glu	Glu	Gln	Ile	Arg	Lys	Lys	Lys	Ile	Arg	Lys	Gln	Gln	Gln	Glu	
			165					170						175		
Ser	Gln	Ser	Gln	Ser	Gln	Ser	Pro	Val	Gly	Pro	Gln	Gly	Ser	Ser	Ser	
		180					185						190			
Ser	Ala	Ser	Gly	Pro	Gly	Ala	Ser	Pro	Gly	Gly	Ser	Glu	Ala	Gly	Ser	
		195					200					205				
Gln	Gly	Ser	Gly	Glu	Gly	Glu	Gly	Val	Gln	Leu	Thr	Ala	Ala	Gln	Glu	
	210					215					220					
Leu	Met	Ile	Gln	Gln	Leu	Val	Ala	Ala	Gln	Leu	Gln	Cys	Asn	Lys	Arg	

225	Ser	Phe	Ser	Asp	Gln	Pro	Lys	Val	Thr	Pro	Trp	Pro	Leu	Gly	Ala	Asp	240
					245					250						255	
	Pro	Gln	Ser	Arg	Asp	Ala	Arg	Gln	Gln	Arg	Phe	Ala	His	Phe	Thr	Glu	
				260					265					270			
	Leu	Ala	Ile	Ile	Ser	Val	Gln	Glu	Ile	Val	Asp	Phe	Ala	Lys	Gln	Val	
			275					280					285				
	Pro	Gly	Phe	Leu	Gln	Leu	Gly	Arg	Glu	Asp	Gln	Ile	Ala	Leu	Leu	Lys	
		290					295					300					
	Ala	Ser	Thr	Ile	Glu	Ile	Met	Leu	Leu	Glu	Thr	Ala	Arg	Arg	Tyr	Asn	
305						310					315					320	
	His	Glu	Thr	Glu	Cys	Ile	Thr	Phe	Leu	Lys	Asp	Phe	Thr	Tyr	Ser	Lys	
				325						330					335		
	Asp	Asp	Phe	His	Arg	Ala	Gly	Leu	Gln	Val	Glu	Phe	Ile	Asn	Pro	Ile	
				340					345					350			
	Phe	Glu	Phe	Ser	Arg	Ala	Met	Arg	Arg	Leu	Gly	Leu	Asp	Asp	Ala	Glu	
			355					360					365				
	Tyr	Ala	Leu	Leu	Ile	Ala	Ile	Asn	Ile	Phe	Ser	Ala	Asp	Arg	Pro	Asn	
		370					375					380					
	Val	Gln	Glu	Pro	Gly	Arg	Val	Glu	Ala	Leu	Gln	Gln	Pro	Tyr	Val	Glu	
385						390					395					400	
	Ala	Leu	Leu	Ser	Tyr	Thr	Arg	Ile	Lys	Arg	Pro	Gln	Asp	Gln	Leu	Arg	
				405					410						415		
	Phe	Pro	Arg	Met	Leu	Met	Lys	Leu	Val	Ser	Leu	Arg	Thr	Leu	Ser	Ser	
				420					425					430			
	Val	His	Ser	Glu	Gln	Val	Phe	Ala	Leu	Arg	Leu	Gln	Asp	Lys	Lys	Leu	
			435				440					445					
	Pro	Pro	Leu	Leu	Ser	Glu	Ile	Trp	Asp	Val	His	Glu					
		450					455					460					

<210> 5  
 <211> 2070  
 <212> DNA  
 <213> Rattus norvegicus

<220>  
 <221> CDS  
 <222> (172) ... (1581)

<300>  
 <308> GeneBank U18374  
 <309> 1995-06-21

<400> 5  
 ctgagttctg agcgtctaca gcgaaagtgc tgggcttttg aaaggagacc tgggctccga 60  
 atcctctcag ggccttggac gtctctgacc caaaacaatc caaggttctt atttgaagac 120  
 caccatccca gaagcacatt ctcgagttga aaagttggag tgggtgttcga a atg aat 177  
 Met Asn  
 1

ctg att ggg ccc tcc cat tta caa gcc acg gac gag ttt gct ctt tct 225  
 Leu Ile Gly Pro Ser His Leu Gln Ala Thr Asp Glu Phe Ala Leu Ser  
 5 10 15

gaa aac tta ttt gga gtg cta aca gag cac gcg gca ggt cct ctg ggg 273  
 Glu Asn Leu Phe Gly Val Leu Thr Glu His Ala Ala Gly Pro Leu Gly  
 20 25 30

cag aat ctg gac ttg gaa tcg tac tcc cca tac aac aat gtg cag ttt 321  
 Gln Asn Leu Asp Leu Glu Ser Tyr Ser Pro Tyr Asn Asn Val Gln Phe  
 35 40 45 50

cct caa gtt cag cca cag atc tcc tcc tcg tcc tat tat tcc aac ctg 369  
 Pro Gln Val Gln Pro Gln Ile Ser Ser Ser Ser Tyr Tyr Ser Asn Leu  
 55 60 65

ggt	ttc	tac	ccg	caa	caa	ccg	gaa	gac	tgg	tac	tct	cct	gga	ctc	tat	417
Gly	Phe	Tyr	Pro	Gln	Gln	Pro	Glu	Asp	Trp	Tyr	Ser	Pro	Gly	Leu	Tyr	
			70					75					80			
gaa	ctc	agg	cga	atg	ccc	act	gag	agt	gtg	tac	cag	gga	gag	act	gag	465
Glu	Leu	Arg	Arg	Met	Pro	Thr	Glu	Ser	Val	Tyr	Gln	Gly	Glu	Thr	Glu	
		85					90					95				
gta	tcc	gag	atg	cct	gtg	aca	aag	aag	ccg	cga	atg	gcc	gcc	tca	tcg	513
Val	Ser	Glu	Met	Pro	Val	Thr	Lys	Lys	Pro	Arg	Met	Ala	Ala	Ser	Ser	
	100					105					110					
gcg	gga	aga	ata	aaa	ggg	gat	gag	ctg	tgt	gtg	gtc	tgc	gga	gac	agg	561
Ala	Gly	Arg	Ile	Lys	Gly	Asp	Glu	Leu	Cys	Val	Val	Cys	Gly	Asp	Arg	
115					120					125					130	
gcc	tct	ggg	tac	cat	tac	aac	gcg	ctc	acc	tgc	gag	ggc	tgc	aaa	ggg	609
Ala	Ser	Gly	Tyr	His	Tyr	Asn	Ala	Leu	Thr	Cys	Glu	Gly	Cys	Lys	Gly	
				135					140					145		
ttc	ttc	cga	aga	agc	atc	acc	aaa	aac	gcc	gtg	tac	aag	tgt	aag	aac	657
Phe	Phe	Arg	Arg	Ser	Ile	Thr	Lys	Asn	Ala	Val	Tyr	Lys	Cys	Lys	Asn	
			150					155					160			
ggg	ggc	aac	tgc	gtg	atg	gat	atg	tac	atg	cgt	cgg	aag	tgc	cag	gat	705
Gly	Gly	Asn	Cys	Val	Met	Asp	Met	Tyr	Met	Arg	Arg	Lys	Cys	Gln	Asp	
		165					170					175				
tgc	cgg	cta	agg	aag	tgc	aga	gag	atg	gga	atg	ttg	gct	gaa	tgt	ttg	753
Cys	Arg	Leu	Arg	Lys	Cys	Arg	Glu	Met	Gly	Met	Leu	Ala	Glu	Cys	Leu	
	180					185					190					
tta	act	gaa	att	cag	tgt	aaa	tct	aaa	cgg	cta	agg	aaa	aat	gtg	aag	801
Leu	Thr	Glu	Ile	Gln	Cys	Lys	Ser	Lys	Arg	Leu	Arg	Lys	Asn	Val	Lys	
195					200					205				210		
cag	cat	gcg	gat	cag	aca	gtg	aat	gag	gac	agc	gaa	ggg	cgt	gac	ttg	849
Gln	His	Ala	Asp	Gln	Thr	Val	Asn	Glu	Asp	Ser	Glu	Gly	Arg	Asp	Leu	
				215					220					225		
cgg	caa	gtg	acc	tcc	acg	acc	aag	cta	tgc	agg	gag	aaa	act	gaa	ctc	897
Arg	Gln	Val	Thr	Ser	Thr	Thr	Lys	Leu	Cys	Arg	Glu	Lys	Thr	Glu	Leu	
			230					235					240			
act	gta	gac	cag	cag	acc	ctc	ctg	gat	tat	att	atg	gac	tca	tac	agc	945
Thr	Val	Asp	Gln	Gln	Thr	Leu	Leu	Asp	Tyr	Ile	Met	Asp	Ser	Tyr	Ser	
		245					250					255				
aaa	cag	aga	atg	cca	cag	gag	atc	aca	aat	aaa	atc	tta	aaa	gaa	gaa	993
Lys	Gln	Arg	Met	Pro	Gln	Glu	Ile	Thr	Asn	Lys	Ile	Leu	Lys	Glu	Glu	
	260					265					270					
ttt	agt	gca	gaa	gaa	aat	ttt	ctc	ata	tta	aca	gaa	atg	gct	acc	agt	1041
Phe	Ser	Ala	Glu	Glu	Asn	Phe	Leu	Ile	Leu	Thr	Glu	Met	Ala	Thr	Ser	
275					280					285					290	
cac	gta	cag	att	ctc	gta	gaa	ttc	aca	aaa	aga	ctt	cca	ggg	ttt	cag	1089
His	Val	Gln	Ile	Leu	Val	Glu	Phe	Thr	Lys	Arg	Leu	Pro	Gly	Phe	Gln	
				295					300					305		
aca	ctg	gac	cac	gaa	gac	cag	att	gct	ttg	ctc	aaa	ggg	tcc	gca	gtc	1137
Thr	Leu	Asp	His	Glu	Asp	Gln	Ile	Ala	Leu	Leu	Lys	Gly	Ser	Ala	Val	
			310					315					320			
gag	gcc	atg	ttc	ctt	cgt	tca	gcg	gag	att	ttc	aat	aag	aaa	ctt	cct	1185
Glu	Ala	Met	Phe	Leu	Arg	Ser	Ala	Glu	Ile	Phe	Asn	Lys	Lys	Leu	Pro	
		325					330					335				



gcc gga cac gca gac ctg ttg gaa gaa aga att cga aag agc ggc atc 1233  
 Ala Gly His Ala Asp Leu Leu Glu Glu Arg Ile Arg Lys Ser Gly Ile  
 340 345 350  
 tcc gat gag tac ata acc ccg atg ttt agt ttc tat aaa agt gtc ggg 1281  
 Ser Asp Glu Tyr Ile Thr Pro Met Phe Ser Phe Tyr Lys Ser Val Gly  
 355 360 365 370  
 gag ctg aaa atg acc cag gaa gag tac gct ctg ctc aca gca att gtc 1329  
 Glu Leu Lys Met Thr Gln Glu Glu Tyr Ala Leu Leu Thr Ala Ile Val  
 375 380 385  
 atc ctc tct cca gac aga caa tac ata aag gat aga gag gca gtg gag 1377  
 Ile Leu Ser Pro Asp Arg Gln Tyr Ile Lys Asp Arg Glu Ala Val Glu  
 390 395 400  
 aag ctt cag gag cct ctg ctc gat gtc cta caa aaa ctc tgc aag atc 1425  
 Lys Leu Gln Glu Pro Leu Leu Asp Val Leu Gln Lys Leu Cys Lys Ile  
 405 410 415  
 tac cag ccc gag aac cct cag cat ttc gcc tgc ctc ctg ggt cgc ctg 1473  
 Tyr Gln Pro Glu Asn Pro Gln His Phe Ala Cys Leu Leu Gly Arg Leu  
 420 425 430  
 aca gaa ctc cgg aca ttc aac cat cac cac gct gag atg ctg atg tct 1521  
 Thr Glu Leu Arg Thr Phe Asn His His His Ala Glu Met Leu Met Ser  
 435 440 445 450  
 tgg agg gtg aat gac cac aag ttc acc ccg ctc ctc tgt gag atc tgg 1569  
 Trp Arg Val Asn Asp His Lys Phe Thr Pro Leu Leu Cys Glu Ile Trp  
 455 460 465  
 gat gtg cag tga aggacacggg gagaggctag ctccttgtcc tcctcagagc 1621  
 Asp Val Gln \*

agcaacctgg tattggactt cccttctttt catttgtacc aggtctcact caagaatctc 1681  
 aatgaatatt tatgtggcaa ttatacaatt cccacaactg taaatacagg ctccatagaa 1741  
 ttgcttcccc tacactgtat tttacaaggc ttcgggaaac cccactgaca cgcccttttt 1801  
 gcctcattaa atcaattgtt acttcaattt tgtcaactga gctagggacc gcctcgtttt 1861  
 atcctccatg cggcaacatt atatatatat atattttatc aaatagctgt tttctcttcc 1921  
 tttttttttt tttttttttt cggagctggg gactgaaccc agggccttgc gcttgctagg 1981  
 caagcgctct accactgagc taaatcccca acccctatta aatagctgtt ttcaactgag 2041  
 acaataaact gaacgtaatg ccaagagaa 2070

<210> 6  
 <211> 469  
 <212> PRT  
 <213> Rattus norvegicus

<400> 6  
 Met Asn Leu Ile Gly Pro Ser His Leu Gln Ala Thr Asp Glu Phe Ala  
 1 5 10 15  
 Leu Ser Glu Asn Leu Phe Gly Val Leu Thr Glu His Ala Ala Gly Pro  
 20 25 30  
 Leu Gly Gln Asn Leu Asp Leu Glu Ser Tyr Ser Pro Tyr Asn Asn Val  
 35 40 45  
 Gln Phe Pro Gln Val Gln Pro Gln Ile Ser Ser Ser Ser Tyr Tyr Ser  
 50 55 60  
 Asn Leu Gly Phe Tyr Pro Gln Gln Pro Glu Asp Trp Tyr Ser Pro Gly  
 65 70 75 80  
 Leu Tyr Glu Leu Arg Arg Met Pro Thr Glu Ser Val Tyr Gln Gly Glu  
 85 90 95  
 Thr Glu Val Ser Glu Met Pro Val Thr Lys Lys Pro Arg Met Ala Ala  
 100 105 110  
 Ser Ser Ala Gly Arg Ile Lys Gly Asp Glu Leu Cys Val Val Cys Gly

Asp	Arg	115	Ala	Ser	Gly	Tyr	His	120	Tyr	Asn	Ala	Leu	Thr	125	Cys	Glu	Gly	Cys
130	Lys	Gly	Phe	Phe	Arg	Arg	Ser	135	Ile	Thr	Lys	Asn	140	Ala	Val	Tyr	Lys	Cys
145	Lys	Asn	Gly	Gly	Asn	Cys	Val	150	Met	Asp	Met	Tyr	155	Met	Arg	Arg	Lys	Cys
				165									170				175	
Gln	Asp	Cys	Arg	Leu	Arg	Lys	Cys	185	Arg	Glu	Met	Gly	190	Met	Leu	Ala	Glu	
Cys	Leu	Leu	Thr	Glu	Ile	Gln	Cys	200	Lys	Ser	Lys	Arg	205	Leu	Arg	Lys	Asn	
Val	Lys	Gln	His	Ala	Asp	Gln	Thr	215	Val	Asn	Glu	Asp	220	Ser	Glu	Gly	Arg	
225	Asp	Leu	Arg	Gln	Val	Thr	Ser	230	Thr	Thr	Lys	Leu	235	Cys	Arg	Glu	Lys	Thr
Glu	Leu	Thr	Val	Asp	Gln	Gln	Thr	245	Leu	Leu	Asp	Tyr	250	Ile	Met	Asp	Ser	
Tyr	Ser	Lys	Gln	Arg	Met	Pro	Gln	260	Glu	Ile	Thr	Asn	265	Lys	Ile	Leu	Lys	
Glu	Glu	Phe	Ser	Ala	Glu	Glu	Asn	275	Phe	Leu	Ile	Leu	280	Thr	Glu	Met	Ala	
Thr	Ser	His	Val	Gln	Ile	Leu	Val	285	Glu	Phe	Thr	Lys	290	Arg	Leu	Pro	Gly	
Phe	Gln	Thr	Leu	Asp	His	Glu	Asp	295	Gln	Ile	Ala	Leu	300	Leu	Lys	Gly	Ser	
305	Ala	Val	Glu	Ala	Met	Phe	Leu	310	Arg	Ser	Ala	Glu	315	Ile	Phe	Asn	Lys	Lys
				325									330				335	
Leu	Pro	Ala	Gly	His	Ala	Asp	Leu	340	Leu	Glu	Glu	Arg	345	Ile	Arg	Lys	Ser	
Gly	Ile	Ser	Asp	Glu	Tyr	Ile	Thr	355	Pro	Met	Phe	Ser	360	Phe	Tyr	Lys	Ser	
Val	Gly	Glu	Leu	Lys	Met	Thr	Gln	365	Glu	Glu	Tyr	Ala	370	Leu	Leu	Thr	Ala	
Ile	Val	Ile	Leu	Ser	Pro	Asp	Arg	375	Gln	Tyr	Ile	Lys	380	Asp	Arg	Glu	Ala	
385	Val	Glu	Lys	Leu	Gln	Glu	Pro	390	Leu	Leu	Asp	Val	395	Leu	Gln	Lys	Leu	Cys
				405									410				415	
Lys	Ile	Tyr	Gln	Pro	Glu	Asn	Pro	420	Gln	His	Phe	Ala	425	Cys	Leu	Leu	Gly	
Arg	Leu	Thr	Glu	Leu	Arg	Thr	Phe	430	Asn	His	His	His	435	Ala	Glu	Met	Leu	
Met	Ser	Trp	Arg	Val	Asn	Asp	His	440	Lys	Phe	Thr	Pro	445	Leu	Leu	Cys	Glu	
Ile	Trp	Asp	Val	Gln				450					455					
465													460					

<210> 7  
 <211> 2218  
 <212> DNA  
 <213> Homo Sapien

<220>  
 <221> CDS  
 <222> (354)...(1772)

<300>  
 <308> GeneBank NM\_005123  
 <309> 2002-11-05

<400> 7  
 acgagactct ctcctcctcc tcacctcatt gtctcccccga cttatcctaa tgcgaaattg 60  
 gattctgagc attttagca aaatcgctgg gatctggaga ggaagactca gtccagaatc 120  
 ctcccagggc cttgaaagtc catctctgac ccaaaacaat ccaaggaggt agaagacatc 180  
 gtagaaggag tgaaagaaga aaagaagact tagaaacata gctcaaagtg aacactgctt 240  
 ctcttagttt cctggatttc ttctggacat ttcctcaaga tgaaacttca gacactttgg 300  
 agtttttttt gaagaccacc ataaagaaag tgcattttcaa ttgaaaaatt tgg atg 356

															Met 1	
gga Gly	tca Ser	aaa Lys	atg Met 5	aat Asn	ctc Leu	att Ile	gaa Glu	cat His 10	tcc Ser	cat His	tta Leu	cct Pro	acc Thr 15	aca Thr	gat Asp	404
gaa Glu	ttt Phe	tct Ser 20	ttt Phe	tct Ser	gaa Glu	aat Asn	tta Leu 25	ttt Phe	ggg Gly	gtt Val	tta Leu	aca Thr 30	gaa Glu	caa Gln	gtg Val	452
gca Ala	ggg Gly 35	cct Pro	ctg Leu	gga Gly	cag Gln	aac Asn 40	ctg Leu	gaa Glu	gtg Val	gaa Glu	cca Pro 45	tac Tyr	tcg Ser	caa Gln	tac Tyr	500
agc Ser 50	aat Asn	gtt Val	cag Gln	ttt Phe	ccc Pro 55	caa Gln	gtt Val	caa Gln	cca Pro	cag Gln 60	att Ile	tcc Ser	tcg Ser	tca Ser	tcc Ser 65	548
tat Tyr	tat Tyr	tcc Ser	aac Asn	ctg Leu 70	ggg Gly	ttc Phe	tac Tyr	ccc Pro	cag Gln 75	cag Gln	cct Pro	gaa Glu	gag Glu	tgg Trp 80	tac Tyr	596
tct Ser	cct Pro	gga Gly	ata Ile 85	tat Tyr	gaa Glu	ctc Leu	agg Arg	cgt Arg 90	atg Met	cca Pro	gct Ala	gag Glu	act Thr 95	ctc Leu	tac Tyr	644
cag Gln	gga Gly	gaa Glu 100	act Thr	gag Glu	gta Val	gca Ala	gag Glu 105	atg Met	cct Pro	gta Val	aca Thr	aag Lys 110	aag Lys	ccc Pro	cgc Arg	692
atg Met	ggc Gly 115	gcg Ala	tca Ser	gca Ala	ggg Gly	agg Arg 120	atc Ile	aaa Lys	ggg Gly	gat Asp	gag Glu 125	ctg Leu	tgt Cys	gtt Val	gtt Val	740
tgt Cys 130	gga Gly	gac Asp	aga Arg	gcc Ala	tct Ser 135	gga Gly	tac Tyr	cac His	tat Tyr	aat Asn 140	gca Ala	ctg Leu	acc Thr	tgt Cys	gag Glu 145	788
ggg Gly	tgt Cys	aaa Lys	ggg Gly	ttc Phe 150	ttc Phe	agg Arg	aga Arg	agc Ser	att Ile 155	acc Thr	aaa Lys	aac Asn	gct Ala	gtg Val 160	tac Tyr	836
aag Lys	tgt Cys	aaa Lys	aac Asn 165	ggg Gly	ggc Gly	aac Asn	tgt Cys	gtg Val 170	atg Met	gat Asp	atg Met	tac Tyr	atg Met 175	cga Arg	aga Arg	884
aag Lys	tgt Cys	caa Gln 180	gag Glu	tgt Cys	cga Arg	cta Leu	agg Arg 185	aaa Lys	tgc Cys	aaa Lys	gag Glu	atg Met 190	gga Gly	atg Met	ttg Leu	932
gct Ala	gaa Glu 195	tgc Cys	ttg Leu	tta Leu	act Thr	gaa Glu 200	att Ile	cag Gln	tgt Cys	aaa Lys	tct Ser 205	aag Lys	cga Arg	ctg Leu	aga Arg	980
aaa Lys 210	aat Asn	gtg Val	aag Lys	cag Gln	cat His 215	gca Ala	gat Asp	cag Gln	acc Thr	gtg Val 220	aat Asn	gaa Glu	gac Asp	agt Ser	gaa Glu 225	1028
ggg Gly	cgt Arg	gac Asp	ttg Leu	cga Arg 230	caa Gln	gtg Val	acc Thr	tcg Ser	aca Thr 235	aca Thr	aag Lys	tca Ser	tgc Cys	agg Arg 240	gag Glu	1076
aaa Lys	act Thr	gaa Glu	ctc Leu 245	acc Thr	cca Pro	gat Asp	caa Gln	cag Gln 250	act Thr	ctt Leu	cta Leu	cat His	ttt Phe 255	att Ile	atg Met	1124

gat tca tat aac aaa cag agg atg cct cag gaa ata aca aat aaa att	1172
Asp Ser Tyr Asn Lys Gln Arg Met Pro Gln Glu Ile Thr Asn Lys Ile	
260 265 270	
tta aaa gaa gaa ttc agt gca gaa gaa aat ttt ctc att ttg acg gaa	1220
Leu Lys Glu Glu Phe Ser Ala Glu Glu Asn Phe Leu Ile Leu Thr Glu	
275 280 285	
atg gca acc aat cat gta cag gtt ctt gta gaa ttc aca aaa aag cta	1268
Met Ala Thr Asn His Val Gln Val Leu Val Glu Phe Thr Lys Lys Leu	
290 295 300 305	
cca gga ttt cag act ttg gac cat gaa gac cag att gct ttg ctg aaa	1316
Pro Gly Phe Gln Thr Leu Asp His Glu Asp Gln Ile Ala Leu Leu Lys	
310 315 320	
ggg tct gcg gtt gaa gct atg ttc ctt cgt tca gct gag att ttc aat	1364
Gly Ser Ala Val Glu Ala Met Phe Leu Arg Ser Ala Glu Ile Phe Asn	
325 330 335	
aag aaa ctt ccg tct ggg cat tct gac cta ttg gaa gaa aga att cga	1412
Lys Lys Leu Pro Ser Gly His Ser Asp Leu Leu Glu Glu Arg Ile Arg	
340 345 350	
aat agt ggt atc tct gat gaa tat ata aca cct atg ttt agt ttt tat	1460
Asn Ser Gly Ile Ser Asp Glu Tyr Ile Thr Pro Met Phe Ser Phe Tyr	
355 360 365	
aaa agt att ggg gaa ctg aaa atg act caa gag gag tat gct ctg ctt	1508
Lys Ser Ile Gly Glu Leu Lys Met Thr Gln Glu Glu Tyr Ala Leu Leu	
370 375 380 385	
aca gca att gtt atc ctg tct cca gat aga caa tac ata aag gat aga	1556
Thr Ala Ile Val Ile Leu Ser Pro Asp Arg Gln Tyr Ile Lys Asp Arg	
390 395 400	
gag gca gta gag aag ctt cag gag cca ctt ctt gat gtg cta caa aag	1604
Glu Ala Val Glu Lys Leu Gln Glu Pro Leu Leu Asp Val Leu Gln Lys	
405 410 415	
ttg tgt aag att cac cag cct gaa aat cct caa cac ttt gcc tgt ctc	1652
Leu Cys Lys Ile His Gln Pro Glu Asn Pro Gln His Phe Ala Cys Leu	
420 425 430	
ctg ggt cgc ctg act gaa tta cgg aca ttc aat cat cac cac gct gag	1700
Leu Gly Arg Leu Thr Glu Leu Arg Thr Phe Asn His His His Ala Glu	
435 440 445	
atg ctg atg tca tgg aga gta aac gac cac aag ttt acc cca ctt ctc	1748
Met Leu Met Ser Trp Arg Val Asn Asp His Lys Phe Thr Pro Leu Leu	
450 455 460 465	
tgt gaa atc tgg gac gtg cag tga tggggattac agggggagggg tctagctcct	1802
Cys Glu Ile Trp Asp Val Gln *	
470	
ttttctctct catattaatc tgatgtataa ctttcttcta tttcacttgt acccagtttc	1862
actcaagaaaa tcttgatgaa tatttatgtt gtaattacat gtgtaacttc cacaactgta	1922
aatattgggc tagatagaac aactttctct acatttgtgt ttaaaaaggct ccagggaatc	1982
ctgcattcta attggcaagc cctgtttgcc taattaaatt gattgttact tcaattctat	2042
ctgttgaaact agggaaaatc tcatTTTgtc catcttacca tattgcatat attttattaa	2102
agagttgtat tcaatcttgg caataaagca aacataatgg caacagaaaa aaaaaaaaaa	2162
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa	2218

<210> 8  
 <211> 472  
 <212> PRT

<213> Homo Sapien

<400> 8

Met	Gly	Ser	Lys	Met	Asn	Leu	Ile	Glu	His	Ser	His	Leu	Pro	Thr	Thr	
1				5					10					15		
Asp	Glu	Phe	Ser	Phe	Ser	Glu	Asn	Leu	Phe	Gly	Val	Leu	Thr	Glu	Gln	
			20					25					30			
Val	Ala	Gly	Pro	Leu	Gly	Gln	Asn	Leu	Glu	Val	Glu	Pro	Tyr	Ser	Gln	
		35				40						45				
Tyr	Ser	Asn	Val	Gln	Phe	Pro	Gln	Val	Gln	Pro	Gln	Ile	Ser	Ser	Ser	
	50				55						60					
Ser	Tyr	Tyr	Ser	Asn	Leu	Gly	Phe	Tyr	Pro	Gln	Gln	Pro	Glu	Glu	Trp	
65				70					75						80	
Tyr	Ser	Pro	Gly	Ile	Tyr	Glu	Leu	Arg	Arg	Met	Pro	Ala	Glu	Thr	Leu	
				85					90					95		
Tyr	Gln	Gly	Glu	Thr	Glu	Val	Ala	Glu	Met	Pro	Val	Thr	Lys	Lys	Pro	
			100					105					110			
Arg	Met	Gly	Ala	Ser	Ala	Gly	Arg	Ile	Lys	Gly	Asp	Glu	Leu	Cys	Val	
		115				120						125				
Val	Cys	Gly	Asp	Arg	Ala	Ser	Gly	Tyr	His	Tyr	Asn	Ala	Leu	Thr	Cys	
	130					135					140					
Glu	Gly	Cys	Lys	Gly	Phe	Phe	Arg	Arg	Ser	Ile	Thr	Lys	Asn	Ala	Val	
145				150						155					160	
Tyr	Lys	Cys	Lys	Asn	Gly	Gly	Asn	Cys	Val	Met	Asp	Met	Tyr	Met	Arg	
				165					170					175		
Arg	Lys	Cys	Gln	Glu	Cys	Arg	Leu	Arg	Lys	Cys	Lys	Glu	Met	Gly	Met	
			180					185					190			
Leu	Ala	Glu	Cys	Leu	Leu	Thr	Glu	Ile	Gln	Cys	Lys	Ser	Lys	Arg	Leu	
		195					200					205				
Arg	Lys	Asn	Val	Lys	Gln	His	Ala	Asp	Gln	Thr	Val	Asn	Glu	Asp	Ser	
	210				215						220					
Glu	Gly	Arg	Asp	Leu	Arg	Gln	Val	Thr	Ser	Thr	Thr	Lys	Ser	Cys	Arg	
225				230						235					240	
Glu	Lys	Thr	Glu	Leu	Thr	Pro	Asp	Gln	Gln	Thr	Leu	Leu	His	Phe	Ile	
				245				250						255		
Met	Asp	Ser	Tyr	Asn	Lys	Gln	Arg	Met	Pro	Gln	Glu	Ile	Thr	Asn	Lys	
			260					265					270			
Ile	Leu	Lys	Glu	Glu	Phe	Ser	Ala	Glu	Glu	Asn	Phe	Leu	Ile	Leu	Thr	
		275					280					285				
Glu	Met	Ala	Thr	Asn	His	Val	Gln	Val	Leu	Val	Glu	Phe	Thr	Lys	Lys	
	290			295							300					
Leu	Pro	Gly	Phe	Gln	Thr	Leu	Asp	His	Glu	Asp	Gln	Ile	Ala	Leu	Leu	
305				310						315					320	
Lys	Gly	Ser	Ala	Val	Glu	Ala	Met	Phe	Leu	Arg	Ser	Ala	Glu	Ile	Phe	
			325					330					335			
Asn	Lys	Lys	Leu	Pro	Ser	Gly	His	Ser	Asp	Leu	Leu	Glu	Glu	Arg	Ile	
			340					345					350			
Arg	Asn	Ser	Gly	Ile	Ser	Asp	Glu	Tyr	Ile	Thr	Pro	Met	Phe	Ser	Phe	
		355					360					365				
Tyr	Lys	Ser	Ile	Gly	Glu	Leu	Lys	Met	Thr	Gln	Glu	Glu	Tyr	Ala	Leu	
	370				375						380					
Leu	Thr	Ala	Ile	Val	Ile	Leu	Ser	Pro	Asp	Arg	Gln	Tyr	Ile	Lys	Asp	
385				390						395					400	
Arg	Glu	Ala	Val	Glu	Lys	Leu	Gln	Glu	Pro	Leu	Leu	Asp	Val	Leu	Gln	
			405					410						415		
Lys	Leu	Cys	Lys	Ile	His	Gln	Pro	Glu	Asn	Pro	Gln	His	Phe	Ala	Cys	
			420					425					430			
Leu	Leu	Gly	Arg	Leu	Thr	Glu	Leu	Arg	Thr	Phe	Asn	His	His	His	Ala	
		435				440						445				
Glu	Met	Leu	Met	Ser	Trp	Arg	Val	Asn	Asp	His	Lys	Phe	Thr	Pro	Leu	
	450					455					460					
Leu	Cys	Glu	Ile	Trp	Asp	Val	Gln									
465					470											

<210> 9

<211> 5449

<212> DNA  
 <213> Homo Sapien

<220>  
 <221> CDS  
 <222> (69)...(1457)

<300>  
 <308> GeneBank NM\_002957  
 <309> 2002-06-21

```

<400> 9
gcgccggggg cgcgcgcgcc cgcgcgccgc tgccctgcgcc gccggccggg catgagttag 60
tcgcagac atg gac acc aaa cat ttc ctg ccg ctc gat ttc tcc acc cag 110
      Met Asp Thr Lys His Phe Leu Pro Leu Asp Phe Ser Thr Gln
        1           5           10

gtg aac tcc tcc ctc acc tcc ccg acg ggg cga ggc tcc atg gct gcc 158
Val Asn Ser Ser Leu Thr Ser Pro Thr Gly Arg Gly Ser Met Ala Ala
  15           20           25           30

ccc tcg ctg cac ccg tcc ctg ggg cct ggc atc ggc tcc ccg gga cag 206
Pro Ser Leu His Pro Ser Leu Gly Pro Gly Ile Gly Ser Pro Gly Gln
           35           40           45

ctg cat tct ccc atc agc acc ctg agc tcc ccc atc aac ggc atg ggc 254
Leu His Ser Pro Ile Ser Thr Leu Ser Ser Pro Ile Asn Gly Met Gly
           50           55           60

ccg cct ttc tcg gtc atc agc tcc ccc atg ggc ccc cac tcc atg tcg 302
Pro Pro Phe Ser Val Ile Ser Ser Pro Met Gly Pro His Ser Met Ser
           65           70           75

gtg ccc acc aca ccc acc ctg ggc ttc agc act ggc agc ccc cag ctc 350
Val Pro Thr Thr Pro Thr Leu Gly Phe Ser Thr Gly Ser Pro Gln Leu
  80           85           90

agc tca cct atg aac ccc gtc agc agc agc gag gac atc aag ccc ccc 398
Ser Ser Pro Met Asn Pro Val Ser Ser Ser Ser Glu Asp Ile Lys Pro Pro
  95           100           105           110

ctg ggc ctc aat ggc gtc ctc aag gtc ccc gcc cac ccc tca gga aac 446
Leu Gly Leu Asn Gly Val Leu Lys Val Pro Ala His Pro Ser Gly Asn
           115           120           125

atg gct tcc ttc acc aag cac atc tgc gcc atc tgc ggg gac cgc tcc 494
Met Ala Ser Phe Thr Lys His Ile Cys Ala Ile Cys Gly Asp Arg Ser
           130           135           140

tca ggc aag cac tat gga gtg tac agc tgc gag ggg tgc aag ggc ttc 542
Ser Gly Lys His Tyr Gly Val Tyr Ser Cys Glu Gly Cys Lys Gly Phe
           145           150           155

ttc aag cgg acg gtg cgc aag gac ctg acc tac acc tgc cgc gac aac 590
Phe Lys Arg Thr Val Arg Lys Asp Leu Thr Tyr Thr Cys Arg Asp Asn
           160           165           170

aag gac tgc ctg att gac aag cgg cag cgg aac cgg tgc cag tac tgc 638
Lys Asp Cys Leu Ile Asp Lys Arg Gln Arg Asn Arg Cys Gln Tyr Cys
           175           180           185           190

cgc tac cag aag tgc ctg gcc atg ggc atg aag cgg gaa gcc gtg cag 686
Arg Tyr Gln Lys Cys Leu Ala Met Gly Met Lys Arg Glu Ala Val Gln
           195           200           205

gag gag cgg cag cgt ggc aag gac cgg aac gag aat gag gtg gag tcg 734
Glu Glu Arg Gln Arg Gly Lys Asp Arg Asn Glu Asn Glu Val Glu Ser

```

210	215	220	
acc agc agc gcc aac gag gac atg ccg gtg gag agg atc ctg gag gct Thr Ser Ser Ala Asn Glu Asp Met Pro Val Glu Arg Ile Leu Glu Ala 225 230 235			782
gag ctg gcc gtg gag ccc aag acc gag acc tac gtg gag gca aac atg Glu Leu Ala Val Glu Pro Lys Thr Glu Thr Tyr Val Glu Ala Asn Met 240 245 250			830
ggg ctg aac ccc agc tcg ccg aac gac cct gtc acc aac att tgc caa Gly Leu Asn Pro Ser Ser Pro Asn Asp Pro Val Thr Asn Ile Cys Gln 255 260 265 270			878
gca gcc gac aaa cag ctt ttc acc ctg gtg gag tgg gcc aag cgg atc Ala Ala Asp Lys Gln Leu Phe Thr Leu Val Glu Trp Ala Lys Arg Ile 275 280 285			926
cca cac ttc tca gag ctg ccc ctg gac gac cag gtc atc ctg ctg cgg Pro His Phe Ser Glu Leu Pro Leu Asp Asp Gln Val Ile Leu Leu Arg 290 295 300			974
gca ggc tgg aat gag ctg ctc atc gcc tcc ttc tcc cac cgc tcc atc Ala Gly Trp Asn Glu Leu Leu Ile Ala Ser Phe Ser His Arg Ser Ile 305 310 315			1022
gcc gtg aag gac ggg atc ctc ctg gcc acc ggg ctg cac gtc cac cgg Ala Val Lys Asp Gly Ile Leu Leu Ala Thr Gly Leu His Val His Arg 320 325 330			1070
aac agc gcc cac agc gca ggg gtg ggc gcc atc ttt gac agg gtg ctg Asn Ser Ala His Ser Ala Gly Val Gly Ala Ile Phe Asp Arg Val Leu 335 340 345 350			1118
acg gag ctt gtg tcc aag atg cgg gac atg cag atg gac aag acg gag Thr Glu Leu Val Ser Lys Met Arg Asp Met Gln Met Asp Lys Thr Glu 355 360 365			1166
ctg ggc tgc ctg cgc gcc atc gtc ctc ttt aac cct gac tcc aag ggg Leu Gly Cys Leu Arg Ala Ile Val Leu Phe Asn Pro Asp Ser Lys Gly 370 375 380			1214
ctc tcg aac ccg gcc gag gtg gag gcg ctg agg gag aag gtc tat gcg Leu Ser Asn Pro Ala Glu Val Glu Ala Leu Arg Glu Lys Val Tyr Ala 385 390 395			1262
tcc ttg gag gcc tac tgc aag cac aag tac cca gag cag ccg gga agg Ser Leu Glu Ala Tyr Cys Lys His Lys Tyr Pro Glu Gln Pro Gly Arg 400 405 410			1310
ttc gct aag ctc ttg ctc cgc ctg ccg gct ctg cgc tcc atc ggg ctc Phe Ala Lys Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Gly Leu 415 420 425 430			1358
aaa tgc ctg gaa cat ctc ttc ttc ttc aag ctc atc ggg gac aca ccc Lys Cys Leu Glu His Leu Phe Phe Phe Lys Leu Ile Gly Asp Thr Pro 435 440 445			1406
att gac acc ttc ctt atg gag atg ctg gag gcg ccg cac caa atg act Ile Asp Thr Phe Leu Met Glu Met Leu Glu Ala Pro His Gln Met Thr 450 455 460			1454
tag gcctgcgggc ccattcctttg tgcccacccg ttctggccac cctgcctgga *			1507
cgccagctgt tcttctcagc ctgagccctg tccctgccct tctctgcctg gcctgtttgg			1567

actttggggc	acagcctgtc	actgctctgc	ctaagagatg	tgttgtcacc	ctccttattt	1627
ctgttactac	ttgtctgtgg	cccagggcag	tggcttttct	gaggcagcag	ccttcgtggc	1687
aagaactagc	gtgagcccag	ccagggcgct	ccccaccggg	ctctcaggac	accctgccac	1747
accccacggg	gcttggggcga	ctacaggggtc	ttcggggccc	agccctggag	ctgcaggagt	1807
tgggaacggg	gcttttgttt	ccgttgctgt	ttatcgatgc	tggttttcag	aattcctgtg	1867
tggccctctc	gtctggagtg	acatcttcat	ctgctctgaa	tactggtgcc	cagccagccc	1927
gtgacagctt	ccccctaata	aggaggggac	agctgggggg	gcaagctggt	gtgtcatcag	1987
caaagacctc	agccgcctcg	gggatgagag	gggactcggt	gggcaagcaa	gctgccctgt	2047
gctctgagtg	agggggaagg	tagccccctt	ttccaaagat	aactcacagt	tttgccctcg	2107
agccaatgag	aacatgagct	gccctctgtg	caaggtttct	gggccacctc	caggctgcag	2167
gggggggtca	ctcaccccc	tgttttctct	ctgccttggg	gttctggttt	cagactccc	2227
actccccgtt	cagaccagag	tgccccggcc	cctccccagc	ctgagctctc	tccttgctct	2287
gcgggggtgg	ctgaggcttg	tccttggttt	ctgcagggct	ggccctggct	cgggcagggt	2347
gggggcatcac	cacctcactg	gccttgctgg	aggcacaggg	ctctgcggac	ctgcagccat	2407
ctgtgaggcc	cgcgggggat	ggagggggag	agggtggcct	gttggtttcc	ctcagagggg	2467
gcagggtggc	tggagagaga	ggggctcagg	aactgggagc	ctcgtgggtg	gggcagatgc	2527
tccgcggcct	ggagtggctc	tgccggggca	ttggtgggac	ccctgctcag	gccttctctc	2587
tggctgccag	ttgtgtctaa	aagactcttg	gaatctgaga	accgggagtc	gcagcgccct	2647
cgggcctggg	ccacacgcag	gccctggtgg	gaccacccag	cctggtattg	tccacggaca	2707
gcgttgttca	cccagagcct	tacttgggag	cctcactgaa	cgctgtctct	ggttgaaggt	2767
ggggtggggg	cggggcttgg	ggcctccctg	gtcagcccca	gtgcggcctg	gcgctcctcc	2827
cgcaggctct	gccccggggc	tccggtgggt	cggggccctc	tcaggttgaa	ctcgcctctt	2887
ttgcactgga	aggccctccc	tttggcctga	gtacttttcc	cgttcacgcc	tcagtcccgt	2947
ggacccagcc	tttgtcagtg	gcagggtgct	gaacagaggg	tggatggggg	ggataccgga	3007
gggggtcttg	tcttcccagc	cgcagtctag	gaatgatgcg	gggggggtga	cgctctctcc	3067
atagtccttc	cccacttggg	gcaggggctt	cctcagtggt	gaggggagct	gcctacaggt	3127
tggaccggga	ggcagtggct	tggagaggca	gctttccagc	cttggtgggg	aagaaagtgt	3187
ccattctttg	ccttcctgga	gctcccagcc	agagctgagc	ttaggcaccc	gagtggagcc	3247
tgcagctgag	tctgtgcccc	agacaggctg	tcagagattc	cagaagcctc	tcctccccgc	3307
cgcctccac	ccctgccttt	cagcgttggt	ggtggcccca	gggtggcccc	tgcccgatcc	3367
accgtcctga	ggcagagtgt	tgagcctcat	aacctgtacca	gggtccccgg	cagctggggc	3427
cctcccaggc	actgccagga	agccccagct	gccccgtggc	ggtgtggtgg	aaatggcagg	3487
agggtgcagg	tactcttggg	gccccagcgg	tgggagtgca	aaagacccaa	cgccaacacc	3547
tgggtgccttt	tgcagccagc	gcccacccat	ccgtgccccg	acccttgggg	atgcccgcgg	3607
ctccagagga	aaaagcccag	ggacggggcc	tccgttgccg	ggggtcggct	gcttcttggg	3667
aactttgtcg	tttccggcgc	tggctggctg	gctggctgta	aagcactgaa	gccccccggc	3727
cgccaacccc	tgaagcaga	acctggcctc	cctggccaca	gcagccttac	ccaccgctct	3787
acgtgtcccc	ggcacttccc	gcagccttcc	cgcccccttc	tcacggcctc	tgtagtgtga	3847
cagtgtctgt	ggtttgaaaa	ggtgatgtgt	ggggagtgcg	gctcatcact	gagtagagag	3907
gtagaatttc	tatttaacca	gacctgtagt	agtattacca	atccagttca	attaaggtga	3967
ttttttgtaa	ttattattat	tttgggtggg	caatctttaa	ttttctaaag	atagcactaa	4027
catcagctca	ttagccacct	gtgcctgtcc	ccgccttggc	ccggctggat	gaagcggctt	4087
ccccgcaggg	ccccacttcc	ccagtggctg	cttccctggg	acccagggca	ccccggcacc	4147
ttcaggcacg	ctcctcagct	ggtcacctcc	cggctttggc	gttcagatgg	ggctccttag	4207
gctcaggagt	gaagatgcca	cagagccggg	ctccccatag	ctgcgtcggg	catgcttggg	4267
agctggcctg	ccaggacctt	ccaccctggg	gcctgtgtca	gccgcccggc	ctccgcaccc	4327
tgggaagcaca	cggcctctgg	gaaggacagc	cctgaccttc	ggttttccga	gcacggtgtt	4387
tcccaagaat	tctgggctgg	cggcctgggt	cagtgctggg	agatgacccc	gagccccctc	4447
cogtggggca	cccaggaggg	ccctgccgga	atgtgcagcc	tgtgggtagt	cggctgggtg	4507
ccctgtcgtg	gagctggggg	gcgtgatctg	gtgctcgtcc	acgcagggtg	gtggtgtaaa	4567
catgtatgtg	ctgtacagag	agacgcgtgt	ggagagagcc	gcacaccagc	gccacccagg	4627
aaaggcggag	cggttaccag	tgttttgtgt	ttatttttaa	tcaagacgtt	tcctctgttt	4687
tcctataaat	ttgcttctgt	taagcaagta	cataaggacc	ctcctttggt	gaaatccggg	4747
ttcgaatgaa	tatctcaagg	caggagatgc	atctatttta	agatgctttg	gagcagacag	4807
ctttagccgt	tcccaatcct	tagcaatgcc	ttagctggga	cgcatagcta	atactttaga	4867
gaggatgaca	gatccataaa	gagagtaaa	ataagagaaa	atgtctaaag	catctggaaa	4927
ggtaaaaaaa	aaaaatctat	ttttgtacaa	ttgtaatatt	atccctcatg	tatacttggg	4987
tatgctgggg	ggagggtctg	gactgtttcg	tttctgcttc	tagagattga	ggtgaaagct	5047
tcgtccgaga	aacggccagg	cagacgatgg	cagaggagag	ggctcctgtg	acggcggcga	5107
ggcttggggg	gaaaccgccc	caatgggggt	gtcttccctc	ggggcaggag	ggtgggcctg	5167
aggctttcaa	gggttttctt	ccctttcgag	taatttttaa	agccttgctc	tggtgtgtcc	5227
tgttgccggc	tctggccttc	ctgtgactga	ctgtgaagtg	gcttctccgt	acgattgtct	5287
ctgaacatc	gtggcctcag	tgccagggtg	ttgctggaca	gtagcattag	aattgtggaa	5347
aaggaaacag	caaagggaga	agtgtgagag	gagaaacaaa	atatgagcgt	ttaaaataca	5407
tcgccattca	gttcgttaaa	aaaaaaaaaa	aaaaaaaaaa	aa		5449



<211> 462  
 <212> PRT  
 <213> Homo Sapien

<400> 10

Met	Asp	Thr	Lys	His	Phe	Leu	Pro	Leu	Asp	Phe	Ser	Thr	Gln	Val	Asn	
1				5					10					15		
Ser	Ser	Leu	Thr	Ser	Pro	Thr	Gly	Arg	Gly	Ser	Met	Ala	Ala	Pro	Ser	
			20					25					30			
Leu	His	Pro	Ser	Leu	Gly	Pro	Gly	Ile	Gly	Ser	Pro	Gly	Gln	Leu	His	
		35					40					45				
Ser	Pro	Ile	Ser	Thr	Leu	Ser	Ser	Pro	Ile	Asn	Gly	Met	Gly	Pro	Pro	
	50					55				60						
Phe	Ser	Val	Ile	Ser	Ser	Pro	Met	Gly	Pro	His	Ser	Met	Ser	Val	Pro	
65					70				75						80	
Thr	Thr	Pro	Thr	Leu	Gly	Phe	Ser	Thr	Gly	Ser	Pro	Gln	Leu	Ser	Ser	
				85					90					95		
Pro	Met	Asn	Pro	Val	Ser	Ser	Ser	Glu	Asp	Ile	Lys	Pro	Pro	Leu	Gly	
			100					105					110			
Leu	Asn	Gly	Val	Leu	Lys	Val	Pro	Ala	His	Pro	Ser	Gly	Asn	Met	Ala	
		115					120					125				
Ser	Phe	Thr	Lys	His	Ile	Cys	Ala	Ile	Cys	Gly	Asp	Arg	Ser	Ser	Gly	
	130				135					140						
Lys	His	Tyr	Gly	Val	Tyr	Ser	Cys	Glu	Gly	Cys	Lys	Gly	Phe	Phe	Lys	
145					150					155					160	
Arg	Thr	Val	Arg	Lys	Asp	Leu	Thr	Tyr	Thr	Cys	Arg	Asp	Asn	Lys	Asp	
				165					170					175		
Cys	Leu	Ile	Asp	Lys	Arg	Gln	Arg	Asn	Arg	Cys	Gln	Tyr	Cys	Arg	Tyr	
			180					185					190			
Gln	Lys	Cys	Leu	Ala	Met	Gly	Met	Lys	Arg	Glu	Ala	Val	Gln	Glu	Glu	
		195					200					205				
Arg	Gln	Arg	Gly	Lys	Asp	Arg	Asn	Glu	Asn	Glu	Val	Glu	Ser	Thr	Ser	
	210					215					220					
Ser	Ala	Asn	Glu	Asp	Met	Pro	Val	Glu	Arg	Ile	Leu	Glu	Ala	Glu	Leu	
225					230					235					240	
Ala	Val	Glu	Pro	Lys	Thr	Glu	Thr	Tyr	Val	Glu	Ala	Asn	Met	Gly	Leu	
				245					250					255		
Asn	Pro	Ser	Ser	Pro	Asn	Asp	Pro	Val	Thr	Asn	Ile	Cys	Gln	Ala	Ala	
			260					265					270			
Asp	Lys	Gln	Leu	Phe	Thr	Leu	Val	Glu	Trp	Ala	Lys	Arg	Ile	Pro	His	
		275					280					285				
Phe	Ser	Glu	Leu	Pro	Leu	Asp	Asp	Gln	Val	Ile	Leu	Leu	Arg	Ala	Gly	
	290					295					300					
Trp	Asn	Glu	Leu	Leu	Ile	Ala	Ser	Phe	Ser	His	Arg	Ser	Ile	Ala	Val	
305					310					315					320	
Lys	Asp	Gly	Ile	Leu	Leu	Ala	Thr	Gly	Leu	His	Val	His	Arg	Asn	Ser	
				325					330					335		
Ala	His	Ser	Ala	Gly	Val	Gly	Ala	Ile	Phe	Asp	Arg	Val	Leu	Thr	Glu	
			340					345					350			
Leu	Val	Ser	Lys	Met	Arg	Asp	Met	Gln	Met	Asp	Lys	Thr	Glu	Leu	Gly	
		355					360					365				
Cys	Leu	Arg	Ala	Ile	Val	Leu	Phe	Asn	Pro	Asp	Ser	Lys	Gly	Leu	Ser	
	370					375					380					
Asn	Pro	Ala	Glu	Val	Glu	Ala	Leu	Arg	Glu	Lys	Val	Tyr	Ala	Ser	Leu	
385					390					395					400	
Glu	Ala	Tyr	Cys	Lys	His	Lys	Tyr	Pro	Glu	Gln	Pro	Gly	Arg	Phe	Ala	
				405					410					415		
Lys	Leu	Leu	Leu	Arg	Leu	Pro	Ala	Leu	Arg	Ser	Ile	Gly	Leu	Lys	Cys	
			420					425					430			
Leu	Glu	His	Leu	Phe	Phe	Phe	Lys	Leu	Ile	Gly	Asp	Thr	Pro	Ile	Asp	
		435					440					445				
Thr	Phe	Leu	Met	Glu	Met	Leu	Glu	Ala	Pro	His	Gln	Met	Thr			
	450					455					460					

<210> 11  
 <211> 2081

<212> DNA  
 <213> Mus musculus  
 <220>  
 <221> CDS  
 <222> (167) ... (1573)  
 <300>  
 <308> GeneBank X57638  
 <309> 1991-03-19

```

<400> 11
gtcacagcct aggcctttgct ggggacctga gaaacgctgc cgccaagttg aagttcaagg 60
ccctgccttc cctgtgaact gacgtttgtg gctgggtcaag ttcgggaaca agacgttgct 120
atcacagctt agcgctctgt ggccctgcctg gccacatcca tccaac atg gtg gac 175
                                     Met Val Asp
                                     1

aca gag agc ccc atc tgt cct ctc tcc cca ctg gag gca gat gac ctg 223
Thr Glu Ser Pro Ile Cys Pro Leu Ser Pro Leu Glu Ala Asp Asp Leu
      5                10                15

gaa agt ccc tta tct gaa gaa ttc tta caa gaa atg gga aac att caa 271
Glu Ser Pro Leu Ser Glu Glu Phe Leu Gln Glu Met Gly Asn Ile Gln
      20                25                30                35

gag att tct cag tcc atc ggt gag gag agc tct gga agc ttt ggt ttt 319
Glu Ile Ser Gln Ser Ile Gly Glu Glu Ser Ser Gly Ser Phe Gly Phe
                        40                45                50

gca gac tac cag tac tta gga agc tgt ccg ggc tcc gag ggc tct gtc 367
Ala Asp Tyr Gln Tyr Leu Gly Ser Cys Pro Gly Ser Glu Gly Ser Val
                        55                60                65

atc aca gac acc ctc tct cca cgt tcc agc cct tcc tca gtc agc tgc 415
Ile Thr Asp Thr Leu Ser Pro Arg Ser Ser Pro Ser Ser Val Ser Cys
                        70                75                80

ccc gtg atc ccc gcc agc acg gac gag tcc ccc ggc agt gcc ctg aac 463
Pro Val Ile Pro Ala Ser Thr Asp Glu Ser Pro Gly Ser Ala Leu Asn
      85                90                95

atc gag tgt cga ata tgt ggg gac aag gcc tca ggg tac cac tac gga 511
Ile Glu Cys Arg Ile Cys Gly Asp Lys Ala Ser Gly Tyr His Tyr Gly
      100                105                110                115

gtt cac gca tgt gaa ggc tgt aag ggc ttc ttt cgg cga act att cgg 559
Val His Ala Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Thr Ile Arg
                        120                125                130

ctg aag ctg gtg tac gac aag tgt gat cgg agc tgc aag att cag aag 607
Leu Lys Leu Val Tyr Asp Lys Cys Asp Arg Ser Cys Lys Ile Gln Lys
                        135                140                145

aag aac cgg aac aaa tgc cag tac tgc cgt ttt cac aag tgc ctg tct 655
Lys Asn Arg Asn Lys Cys Gln Tyr Cys Arg Phe His Lys Cys Leu Ser
                        150                155                160

gtc ggg atg tca cac aat gca att cgc ttt gga aga atg cca aga tct 703
Val Gly Met Ser His Asn Ala Ile Arg Phe Gly Arg Met Pro Arg Ser
                        165                170                175

gaa aaa gca aaa ctg aaa gca gaa att ctt acc tgt gaa cac gac ctg 751
Glu Lys Ala Lys Leu Lys Ala Glu Ile Leu Thr Cys Glu His Asp Leu
      180                185                190                195

aaa gat tcg gaa act gca gac ctc aaa tct ctg ggc aag aga atc cac 799

```

Lys	Asp	Ser	Glu	Thr	Ala	Asp	Leu	Lys	Ser	Leu	Gly	Lys	Arg	Ile	His	
				200					205					210		
gaa	gcc	tac	ctg	aag	aac	ttc	aac	atg	aac	aag	gtc	aag	gcc	cgg	gtc	847
Glu	Ala	Tyr	Leu	Lys	Asn	Phe	Asn	Met	Asn	Lys	Val	Lys	Ala	Arg	Val	
			215					220					225			
ata	ctc	gcg	gga	aag	acc	agc	aac	aac	ccg	cct	ttt	gtc	ata	cat	gac	895
Ile	Leu	Ala	Gly	Lys	Thr	Ser	Asn	Asn	Pro	Pro	Phe	Val	Ile	His	Asp	
		230					235					240				
atg	gag	acc	ttg	tgt	atg	gcc	gag	aag	acg	ctt	gtg	gcc	aag	atg	gtg	943
Met	Glu	Thr	Leu	Cys	Met	Ala	Glu	Lys	Thr	Leu	Val	Ala	Lys	Met	Val	
	245					250					255					
gcc	aac	ggc	gtc	gaa	gac	aaa	gag	gca	gag	gtc	cga	ttc	ttc	cac	tgc	991
Ala	Asn	Gly	Val	Glu	Asp	Lys	Glu	Ala	Glu	Val	Arg	Phe	Phe	His	Cys	
260					265					270					275	
tgc	cag	tgc	atg	tcc	gtg	gag	acc	gtc	acg	gag	ctc	aca	gaa	ttt	gcc	1039
Cys	Gln	Cys	Met	Ser	Val	Glu	Thr	Val	Thr	Glu	Leu	Thr	Glu	Phe	Ala	
				280					285					290		
aag	gct	atc	cca	ggc	ttt	gca	aac	ttg	gac	ttg	aac	gac	caa	gtc	acc	1087
Lys	Ala	Ile	Pro	Gly	Phe	Ala	Asn	Leu	Asp	Leu	Asn	Asp	Gln	Val	Thr	
			295					300					305			
ttg	cta	aag	tac	ggc	gtg	tat	gaa	gcc	atc	ttc	acg	atg	ctg	tcc	tcc	1135
Leu	Leu	Lys	Tyr	Gly	Val	Tyr	Glu	Ala	Ile	Phe	Thr	Met	Leu	Ser	Ser	
		310					315					320				
ttg	atg	aac	aaa	gac	ggg	atg	ctg	atc	gcg	tac	ggc	aat	ggc	ttt	atc	1183
Leu	Met	Asn	Lys	Asp	Gly	Met	Leu	Ile	Ala	Tyr	Gly	Asn	Gly	Phe	Ile	
	325					330					335					
aca	cgc	gag	ttc	ctt	aag	aac	ctg	agg	aag	ccg	ttc	tgt	gac	atc	atg	1231
Thr	Arg	Glu	Phe	Leu	Lys	Asn	Leu	Arg	Lys	Pro	Phe	Cys	Asp	Ile	Met	
340					345					350					355	
gaa	ccc	aag	ttt	gac	ttc	gct	atg	aag	ttc	aat	gcc	tta	gaa	ctg	gat	1279
Glu	Pro	Lys	Phe	Asp	Phe	Ala	Met	Lys	Phe	Asn	Ala	Leu	Glu	Leu	Asp	
				360					365					370		
gac	agt	gac	att	tcc	ctg	ttt	gtg	gct	gct	ata	att	tgc	tgt	gga	gat	1327
Asp	Ser	Asp	Ile	Ser	Leu	Phe	Val	Ala	Ala	Ile	Ile	Cys	Cys	Gly	Asp	
			375					380					385			
cgg	cct	ggc	ctt	cta	aac	ata	ggc	tac	att	gag	aag	ttg	cag	gag	ggg	1375
Arg	Pro	Gly	Leu	Leu	Asn	Ile	Gly	Tyr	Ile	Glu	Lys	Leu	Gln	Glu	Gly	
		390					395					400				
att	gtg	cac	gtg	ctt	aag	ctc	cac	ctg	cag	agc	aac	cat	cca	gat	gac	1423
Ile	Val	His	Val	Leu	Lys	Leu	His	Leu	Gln	Ser	Asn	His	Pro	Asp	Asp	
	405					410					415					
acc	ttc	ctc	ttc	cca	aag	ctc	ctt	caa	aaa	atg	gtg	gac	ctt	cgg	cag	1471
Thr	Phe	Leu	Phe	Pro	Lys	Leu	Leu	Gln	Lys	Met	Val	Asp	Leu	Arg	Gln	
420					425					430					435	
ctg	gtc	acg	gag	cat	gcg	cag	ctc	gta	cag	gtc	atc	aag	aag	acc	gag	1519
Leu	Val	Thr	Glu	His	Ala	Gln	Leu	Val	Gln	Val	Ile	Lys	Lys	Thr	Glu	
				440				445						450		
tcc	gac	gca	gcg	ctg	cac	cca	ctg	ttg	caa	gag	atc	tac	aga	gac	atg	1567
Ser	Asp	Ala	Ala	Leu	His	Pro	Leu	Leu	Gln	Glu	Ile	Tyr	Arg	Asp	Met	
			455					460					465			

tac tga tctttcctga gatggcaggc cattaccact gttcagggac ctccgaggcc 1623  
Tyr \*

tgcggcccca tacaggagag cagggatttg cacagagggc ctccctccta cgcttgggga 1683  
tgaagagggc tgagcgtagg taatgcgggc tctccccaca tcctttctga atgggcactt 1743  
ctaagactac ctgctaccga aatgggggtg atcggaggct aataggattc agacagtac 1803  
agacaacggc agtccccagt ctggtcttaa ccggcccaat gttaataaat gcacagcact 1863  
ctacgttgcg ttataaatc gccattaatt aacgggtaac ctccaagtct gagcggctctg 1923  
ttcccttcct gccacccttc tggctatgtg cactctctta aatccctgaa aactaatctg 1983  
cactttttaa cctttgaaaa cctacaagtc aaggtgtggc ccaaggttag ccatttaaat 2043  
gtggcaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa 2081

<210> 12  
<211> 468  
<212> PRT  
<213> Mus musculus

<400> 12  
Met Val Asp Thr Glu Ser Pro Ile Cys Pro Leu Ser Pro Leu Glu Ala  
1 5 10 15  
Asp Asp Leu Glu Ser Pro Leu Ser Glu Glu Phe Leu Gln Glu Met Gly  
20 25 30  
Asn Ile Gln Glu Ile Ser Gln Ser Ile Gly Glu Glu Ser Ser Gly Ser  
35 40 45  
Phe Gly Phe Ala Asp Tyr Gln Tyr Leu Gly Ser Cys Pro Gly Ser Glu  
50 55 60  
Gly Ser Val Ile Thr Asp Thr Leu Ser Pro Arg Ser Ser Pro Ser Ser  
65 70 75 80  
Val Ser Cys Pro Val Ile Pro Ala Ser Thr Asp Glu Ser Pro Gly Ser  
85 90 95  
Ala Leu Asn Ile Glu Cys Arg Ile Cys Gly Asp Lys Ala Ser Gly Tyr  
100 105 110  
His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg  
115 120 125  
Thr Ile Arg Leu Lys Leu Val Tyr Asp Lys Cys Asp Arg Ser Cys Lys  
130 135 140  
Ile Gln Lys Lys Asn Arg Asn Lys Cys Gln Tyr Cys Arg Phe His Lys  
145 150 155 160  
Cys Leu Ser Val Gly Met Ser His Asn Ala Ile Arg Phe Gly Arg Met  
165 170 175  
Pro Arg Ser Glu Lys Ala Lys Leu Lys Ala Glu Ile Leu Thr Cys Glu  
180 185 190  
His Asp Leu Lys Asp Ser Glu Thr Ala Asp Leu Lys Ser Leu Gly Lys  
195 200 205  
Arg Ile His Glu Ala Tyr Leu Lys Asn Phe Asn Met Asn Lys Val Lys  
210 215 220  
Ala Arg Val Ile Leu Ala Gly Lys Thr Ser Asn Asn Pro Pro Phe Val  
225 230 235 240  
Ile His Asp Met Glu Thr Leu Cys Met Ala Glu Lys Thr Leu Val Ala  
245 250 255  
Lys Met Val Ala Asn Gly Val Glu Asp Lys Glu Ala Glu Val Arg Phe  
260 265 270  
Phe His Cys Cys Gln Cys Met Ser Val Glu Thr Val Thr Glu Leu Thr  
275 280 285  
Glu Phe Ala Lys Ala Ile Pro Gly Phe Ala Asn Leu Asp Leu Asn Asp  
290 295 300  
Gln Val Thr Leu Leu Lys Tyr Gly Val Tyr Glu Ala Ile Phe Thr Met  
305 310 315 320  
Leu Ser Ser Leu Met Asn Lys Asp Gly Met Leu Ile Ala Tyr Gly Asn  
325 330 335  
Gly Phe Ile Thr Arg Glu Phe Leu Lys Asn Leu Arg Lys Pro Phe Cys  
340 345 350  
Asp Ile Met Glu Pro Lys Phe Asp Phe Ala Met Lys Phe Asn Ala Leu  
355 360 365  
Glu Leu Asp Asp Ser Asp Ile Ser Leu Phe Val Ala Ala Ile Ile Cys  
370 375 380

Cys Gly Asp Arg Pro Gly Leu Leu Asn Ile Gly Tyr Ile Glu Lys Leu  
 385 390 395 400  
 Gln Glu Gly Ile Val His Val Leu Lys Leu His Leu Gln Ser Asn His  
 405 410 415  
 Pro Asp Asp Thr Phe Leu Phe Pro Lys Leu Leu Gln Lys Met Val Asp  
 420 425 430  
 Leu Arg Gln Leu Val Thr Glu His Ala Gln Leu Val Gln Val Ile Lys  
 435 440 445  
 Lys Thr Glu Ser Asp Ala Ala Leu His Pro Leu Leu Gln Glu Ile Tyr  
 450 455 460  
 Arg Asp Met Tyr  
 465

<210> 13  
 <211> 1323  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> CDS  
 <222> (1)...(1323)  
 <300>  
 <308> GeneBank U10375  
 <309> 1994-07-22

<400> 13  
 atg gaa cag cca cag gag gag acc cct gag gcc cgg gaa gag gag aaa 48  
 Met Glu Gln Pro Gln Glu Glu Thr Pro Glu Ala Arg Glu Glu Lys  
 1 5 10 15  
 gag gaa gtg gcc atg ggt gac gga gcc ccg gag ctc aat ggg gga cca 96  
 Glu Glu Val Ala Met Gly Asp Gly Ala Pro Glu Leu Asn Gly Gly Pro  
 20 25 30  
 gaa cac acg ctt cct tcc agc agc tgt gca gac ctc tcc cag aat tcc 144  
 Glu His Thr Leu Pro Ser Ser Ser Cys Ala Asp Leu Ser Gln Asn Ser  
 35 40 45  
 tcc cct tcc tcc ctg ctg gac cag ctg cag atg ggc tgt gat ggg gcc 192  
 Ser Pro Ser Ser Leu Leu Asp Gln Leu Gln Met Gly Cys Asp Gly Ala  
 50 55 60  
 tca ggc ggc agc ctc aac atg gaa tgt cgg gtg tgc ggg gac aag gcc 240  
 Ser Gly Gly Ser Leu Asn Met Glu Cys Arg Val Cys Gly Asp Lys Ala  
 65 70 75 80  
 tcg ggc ttc cac tac ggg gtc cac gcg tgc gag ggg tgc aag ggc ttc 288  
 Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly Phe  
 85 90 95  
 ttc cgc cgg aca atc cgc atg aag ctc gag tat gag aag tgc gat cgg 336  
 Phe Arg Arg Thr Ile Arg Met Lys Leu Glu Tyr Glu Lys Cys Asp Arg  
 100 105 110  
 atc tgc aag atc cag aag aag aac cgc aac aag tgt cag tac tgc cgc 384  
 Ile Cys Lys Ile Gln Lys Lys Asn Arg Asn Lys Cys Gln Tyr Cys Arg  
 115 120 125  
 ttc cag aag tgc ctg gca ctc ggc atg tcg cac aac gct atc cgc ttt 432  
 Phe Gln Lys Cys Leu Ala Leu Gly Met Ser His Asn Ala Ile Arg Phe  
 130 135 140  
 gga cgg atg ccg gac ggc gag aag agg aag ctg gtg gcg ggg ctg act 480  
 Gly Arg Met Pro Asp Gly Glu Lys Arg Lys Leu Val Ala Gly Leu Thr  
 145 150 155 160

gcc	agc	gag	ggg	tgc	cag	cac	aac	ccc	cag	ctg	gcc	gac	ctg	aag	gcc	528
Ala	Ser	Glu	Gly	Cys	Gln	His	Asn	Pro	Gln	Leu	Ala	Asp	Leu	Lys	Ala	
				165					170					175		
ttc	tct	aag	cac	atc	tac	aac	gcc	tac	ctg	aaa	aac	ttc	aac	atg	acc	576
Phe	Ser	Lys	His	Ile	Tyr	Asn	Ala	Tyr	Leu	Lys	Asn	Phe	Asn	Met	Thr	
			180					185					190			
aaa	aag	aag	gcc	cgg	agc	atc	ctc	acc	ggc	aag	tcc	agc	cac	aac	gca	624
Lys	Lys	Lys	Ala	Arg	Ser	Ile	Leu	Thr	Gly	Lys	Ser	Ser	His	Asn	Ala	
		195					200					205				
ccc	ttt	gtc	atc	cac	gac	atc	gag	aca	ctg	tgg	cag	gca	gag	aag	ggc	672
Pro	Phe	Val	Ile	His	Asp	Ile	Glu	Thr	Leu	Trp	Gln	Ala	Glu	Lys	Gly	
	210					215					220					
ctg	gtg	tgg	aaa	cag	ctg	gtg	aac	ggg	ctg	ccg	ccc	tac	aac	gag	atc	720
Leu	Val	Trp	Lys	Gln	Leu	Val	Asn	Gly	Leu	Pro	Pro	Tyr	Asn	Glu	Ile	
	225				230					235					240	
agt	gtg	cac	gtg	ttc	tac	cgc	tgc	cag	tcc	acc	aca	gtg	gag	aca	gtc	768
Ser	Val	His	Val	Phe	Tyr	Arg	Cys	Gln	Ser	Thr	Thr	Val	Glu	Thr	Val	
				245					250					255		
cga	gag	ctc	acc	gag	ttc	gcc	aag	aac	atc	ccc	aac	ttc	agc	agc	ctc	816
Arg	Glu	Leu	Thr	Glu	Phe	Ala	Lys	Asn	Ile	Pro	Asn	Phe	Ser	Ser	Leu	
			260					265					270			
ttc	ctc	aat	gac	cag	gtg	acc	ctc	ctc	aag	tat	ggc	gtg	cac	gag	gcc	864
Phe	Leu	Asn	Asp	Gln	Val	Thr	Leu	Leu	Lys	Tyr	Gly	Val	His	Glu	Ala	
		275					280					285				
atc	ttt	gcc	atg	ctg	gcc	tcc	atc	gtc	aac	aaa	gac	ggg	ctg	ctg	gtg	912
Ile	Phe	Ala	Met	Leu	Ala	Ser	Ile	Val	Asn	Lys	Asp	Gly	Leu	Leu	Val	
	290					295					300					
gcc	aac	ggc	agt	ggc	ttc	gtc	acc	cac	gag	ttc	ttg	cga	agt	ctc	cgc	960
Ala	Asn	Gly	Ser	Gly	Phe	Val	Thr	His	Glu	Phe	Leu	Arg	Ser	Leu	Arg	
	305				310					315					320	
aag	ccc	ttc	agt	gac	atc	att	gag	ccc	aag	ttc	gag	ttt	gct	gtc	aag	1008
Lys	Pro	Phe	Ser	Asp	Ile	Ile	Glu	Pro	Lys	Phe	Glu	Phe	Ala	Val	Lys	
				325					330					335		
ttc	aat	gcg	ctg	gag	ctc	gat	gac	agt	gac	ctg	gcg	ctc	ttc	atc	gcg	1056
Phe	Asn	Ala	Leu	Glu	Leu	Asp	Asp	Ser	Asp	Leu	Ala	Leu	Phe	Ile	Ala	
			340					345					350			
gcc	atc	att	ctg	tgt	gga	gac	cgg	cca	ggc	ctc	atg	aat	gtg	ccc	cag	1104
Ala	Ile	Ile	Leu	Cys	Gly	Asp	Arg	Pro	Gly	Leu	Met	Asn	Val	Pro	Gln	
		355				360						365				
gta	gaa	gcc	atc	cag	gac	acc	att	ctg	cgg	gct	cta	gaa	ttc	cat	ctg	1152
Val	Glu	Ala	Ile	Gln	Asp	Thr	Ile	Leu	Arg	Ala	Leu	Glu	Phe	His	Leu	
	370					375					380					
cag	gtc	aac	cac	cct	gac	agc	cag	tac	ctc	ttc	ccc	aag	ctg	ctg	cag	1200
Gln	Val	Asn	His	Pro	Asp	Ser	Gln	Tyr	Leu	Phe	Pro	Lys	Leu	Leu	Gln	
	385				390					395					400	
aag	atg	gca	gac	ctg	cgg	cag	ctg	gtc	act	gag	cat	gcc	cag	atg	atg	1248
Lys	Met	Ala	Asp	Leu	Arg	Gln	Leu	Val	Thr	Glu	His	Ala	Gln	Met	Met	
				405				410						415		
cag	tgg	cta	aag	aag	acg	gag	agt	gag	acc	ttg	ctg	cac	ccc	ctg	ctc	1296
Gln	Trp	Leu	Lys	Lys	Thr	Glu	Ser	Glu	Thr	Leu	Leu	His	Pro	Leu	Leu	

420                      425                      430  
 cag gaa atc tac aag gac atg tac taa  
 Gln Glu Ile Tyr Lys Asp Met Tyr \*  
       435                      440

1323

<210> 14  
 <211> 440  
 <212> PRT  
 <213> Mus musculus

<400> 14  
 Met Glu Gln Pro Gln Glu Glu Thr Pro Glu Ala Arg Glu Glu Glu Lys  
   1                  5                  10                  15  
 Glu Glu Val Ala Met Gly Asp Gly Ala Pro Glu Leu Asn Gly Gly Pro  
                   20                  25                  30  
 Glu His Thr Leu Pro Ser Ser Ser Cys Ala Asp Leu Ser Gln Asn Ser  
                   35                  40                  45  
 Ser Pro Ser Ser Leu Leu Asp Gln Leu Gln Met Gly Cys Asp Gly Ala  
                   50                  55                  60  
 Ser Gly Gly Ser Leu Asn Met Glu Cys Arg Val Cys Gly Asp Lys Ala  
   65                  70                  75                  80  
 Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly Phe  
                   85                  90                  95  
 Phe Arg Arg Thr Ile Arg Met Lys Leu Glu Tyr Glu Lys Cys Asp Arg  
                   100                  105                  110  
 Ile Cys Lys Ile Gln Lys Lys Asn Arg Asn Lys Cys Gln Tyr Cys Arg  
                   115                  120                  125  
 Phe Gln Lys Cys Leu Ala Leu Gly Met Ser His Asn Ala Ile Arg Phe  
                   130                  135                  140  
 Gly Arg Met Pro Asp Gly Glu Lys Arg Lys Leu Val Ala Gly Leu Thr  
   145                  150                  155                  160  
 Ala Ser Glu Gly Cys Gln His Asn Pro Gln Leu Ala Asp Leu Lys Ala  
                   165                  170                  175  
 Phe Ser Lys His Ile Tyr Asn Ala Tyr Leu Lys Asn Phe Asn Met Thr  
                   180                  185                  190  
 Lys Lys Lys Ala Arg Ser Ile Leu Thr Gly Lys Ser Ser His Asn Ala  
                   195                  200                  205  
 Pro Phe Val Ile His Asp Ile Glu Thr Leu Trp Gln Ala Glu Lys Gly  
                   210                  215                  220  
 Leu Val Trp Lys Gln Leu Val Asn Gly Leu Pro Pro Tyr Asn Glu Ile  
   225                  230                  235                  240  
 Ser Val His Val Phe Tyr Arg Cys Gln Ser Thr Thr Val Glu Thr Val  
                   245                  250                  255  
 Arg Glu Leu Thr Glu Phe Ala Lys Asn Ile Pro Asn Phe Ser Ser Leu  
                   260                  265                  270  
 Phe Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu Ala  
                   275                  280                  285  
 Ile Phe Ala Met Leu Ala Ser Ile Val Asn Lys Asp Gly Leu Leu Val  
                   290                  295                  300  
 Ala Asn Gly Ser Gly Phe Val Thr His Glu Phe Leu Arg Ser Leu Arg  
   305                  310                  315                  320  
 Lys Pro Phe Ser Asp Ile Ile Glu Pro Lys Phe Glu Phe Ala Val Lys  
                   325                  330                  335  
 Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Leu Phe Ile Ala  
                   340                  345                  350  
 Ala Ile Ile Leu Cys Gly Asp Arg Pro Gly Leu Met Asn Val Pro Gln  
                   355                  360                  365  
 Val Glu Ala Ile Gln Asp Thr Ile Leu Arg Ala Leu Glu Phe His Leu  
                   370                  375                  380  
 Gln Val Asn His Pro Asp Ser Gln Tyr Leu Phe Pro Lys Leu Leu Gln  
   385                  390                  395                  400  
 Lys Met Ala Asp Leu Arg Gln Leu Val Thr Glu His Ala Gln Met Met  
                   405                  410                  415  
 Gln Trp Leu Lys Lys Thr Glu Ser Glu Thr Leu Leu His Pro Leu Leu  
                   420                  425                  430

Gln Glu Ile Tyr Lys Asp Met Tyr  
435 440

<210> 15  
<211> 1827  
<212> DNA  
<213> Homo Sapien

<220>  
<221> CDS  
<222> (292) ... (1683)

<300>  
<308> GeneBank XM\_053680  
<309> 2002-05-08

<400> 15  
gtagcgggtga cggcggcgggc ggcgggcgggc gcagcattat gcgtgattac tgacaggcac 60  
cagctgctgc cgccacagcc gtctcaaacg cactatgtgg actctccgat ctagaggcag 120  
attcctgact aatcccagag ggctggccca gcctgtgctc cccgggctgc taggaagcga 180  
tgaccactct tgtagccca agttgaagaa agccgggctg tgcctgggag ccgagagagg 240  
cggtaaatatt tagaagctgc acaggagagg aacatgaact gacgagtaaa c atg tat 297  
Met Tyr  
1  
  
gga aat tat tct cac ttc atg aag ttt ccc gca ggc tat gga ggc tcc 345  
Gly Asn Tyr Ser His Phe Met Lys Phe Pro Ala Gly Tyr Gly Gly Ser  
5 10 15  
  
cct ggc cac act ggc tct aca tcc atg agc cca tca gca gcc ttg tcc 393  
Pro Gly His Thr Gly Ser Thr Ser Met Ser Pro Ser Ala Ala Leu Ser  
20 25 30  
  
aca ggg aag cca atg gac agc cac ccc agc tac aca gat acc cca gtg 441  
Thr Gly Lys Pro Met Asp Ser His Pro Ser Tyr Thr Asp Thr Pro Val  
35 40 45 50  
  
agt gcc cca cgg act ctg agt gca gtg ggg acc ccc ctc aat gcc ctg 489  
Ser Ala Pro Arg Thr Leu Ser Ala Val Gly Thr Pro Leu Asn Ala Leu  
55 60 65  
  
ggc tct cca tat cga gtc atc acc tct gcc atg ggc cca ccc tca gga 537  
Gly Ser Pro Tyr Arg Val Ile Thr Ser Ala Met Gly Pro Pro Ser Gly  
70 75 80  
  
gca ctt gca gcg cct cca gga atc aac ttg gtt gcc cca ccc agc tct 585  
Ala Leu Ala Ala Pro Pro Gly Ile Asn Leu Val Ala Pro Pro Ser Ser  
85 90 95  
  
cag cta aat gtg gtc aac agt gtc agc agt tca gag gac atc aag ccc 633  
Gln Leu Asn Val Val Asn Ser Val Ser Ser Ser Glu Asp Ile Lys Pro  
100 105 110  
  
tta cca ggg ctt ccc ggg att gga aac atg aac tac cca tcc acc agc 681  
Leu Pro Gly Leu Pro Gly Ile Gly Asn Met Asn Tyr Pro Ser Thr Ser  
115 120 125 130  
  
ccc gga tct ctg gtt aaa cac atc tgt gcc atc tgt gga gac aga tcc 729  
Pro Gly Ser Leu Val Lys His Ile Cys Ala Ile Cys Gly Asp Arg Ser  
135 140 145  
  
tca gga aag cac tac ggg gta tac agt tgt gaa ggc tgc aaa ggg ttc 777  
Ser Gly Lys His Tyr Gly Val Tyr Ser Cys Glu Gly Cys Lys Gly Phe  
150 155 160  
  
ttc aag agg acg ata agg aag gac ctc atc tac acg tgt cgg gat aat 825



Phe	Lys	Arg	Thr	Ile	Arg	Lys	Asp	Leu	Ile	Tyr	Thr	Cys	Arg	Asp	Asn	
		165					170					175				
aaa	gac	tgc	ctc	att	gac	aag	cgt	cag	cgc	aac	cgc	tgc	cag	tac	tgt	873
Lys	Asp	Cys	Leu	Ile	Asp	Lys	Arg	Gln	Arg	Asn	Arg	Cys	Gln	Tyr	Cys	
	180					185					190					
cgc	tat	cag	aag	tgc	ctt	gtc	atg	ggc	atg	aag	agg	gaa	gct	gtg	caa	921
Arg	Tyr	Gln	Lys	Cys	Leu	Val	Met	Gly	Met	Lys	Arg	Glu	Ala	Val	Gln	
195					200					205					210	
gaa	gaa	aga	cag	agg	agc	cga	gag	cga	gct	gag	agt	gag	gca	gaa	tgt	969
Glu	Glu	Arg	Gln	Arg	Ser	Arg	Glu	Arg	Ala	Glu	Ser	Glu	Ala	Glu	Cys	
				215					220					225		
gct	acc	agt	ggg	cat	gaa	gac	atg	cct	gtg	gag	agg	att	cta	gaa	gct	1017
Ala	Thr	Ser	Gly	His	Glu	Asp	Met	Pro	Val	Glu	Arg	Ile	Leu	Glu	Ala	
			230					235					240			
gaa	ctt	gct	gtt	gaa	cca	aag	aca	gaa	tcc	tat	ggg	gac	atg	aat	atg	1065
Glu	Leu	Ala	Val	Glu	Pro	Lys	Thr	Glu	Ser	Tyr	Gly	Asp	Met	Asn	Met	
		245					250					255				
gag	aac	tcg	aca	aat	gac	cct	gtt	acc	aac	ata	tgt	cat	gct	gct	gac	1113
Glu	Asn	Ser	Thr	Asn	Asp	Pro	Val	Thr	Asn	Ile	Cys	His	Ala	Ala	Asp	
	260					265					270					
aag	cag	ctt	ttc	acc	ctc	gtt	gaa	tgg	gcc	aag	cgt	att	ccc	cac	ttc	1161
Lys	Gln	Leu	Phe	Thr	Leu	Val	Glu	Trp	Ala	Lys	Arg	Ile	Pro	His	Phe	
275					280					285					290	
tct	gac	ctc	acc	ttg	gag	gac	cag	gtc	att	ttg	ctt	cgg	gca	ggg	tgg	1209
Ser	Asp	Leu	Thr	Leu	Glu	Asp	Gln	Val	Ile	Leu	Leu	Arg	Ala	Gly	Trp	
				295				300						305		
aat	gaa	ttg	ctg	att	gcc	tct	ttc	tcc	cac	cgc	tca	gtt	tcc	gtg	cag	1257
Asn	Glu	Leu	Leu	Ile	Ala	Ser	Phe	Ser	His	Arg	Ser	Val	Ser	Val	Gln	
			310					315					320			
gat	ggc	atc	ctt	ctg	gcc	acg	ggg	tta	cat	gtc	cac	cgg	agc	agt	gcc	1305
Asp	Gly	Ile	Leu	Leu	Ala	Thr	Gly	Leu	His	Val	His	Arg	Ser	Ser	Ala	
		325					330					335				
cac	agt	gct	ggg	gtc	ggc	tcc	atc	ttt	gac	aga	gtc	cta	act	gag	ctg	1353
His	Ser	Ala	Gly	Val	Gly	Ser	Ile	Phe	Asp	Arg	Val	Leu	Thr	Glu	Leu	
	340					345					350					
gtt	tcc	aaa	atg	aaa	gac	atg	cag	atg	gac	aag	tcg	gaa	ctg	gga	tgc	1401
Val	Ser	Lys	Met	Lys	Asp	Met	Gln	Met	Asp	Lys	Ser	Glu	Leu	Gly	Cys	
355					360					365					370	
ctg	cga	gcc	att	gta	ctc	ttt	aac	cca	gat	gcc	aag	ggc	ctg	tcc	aac	1449
Leu	Arg	Ala	Ile	Val	Leu	Phe	Asn	Pro	Asp	Ala	Lys	Gly	Leu	Ser	Asn	
				375				380						385		
ccc	tct	gag	gtg	gag	act	ctg	cga	gag	aag	gtt	tat	gcc	acc	ctt	gag	1497
Pro	Ser	Glu	Val	Glu	Thr	Leu	Arg	Glu	Lys	Val	Tyr	Ala	Thr	Leu	Glu	
			390					395					400			
gcc	tac	acc	aag	cag	aag	tat	ccg	gaa	cag	cca	ggc	agg	ttt	gcc	aag	1545
Ala	Tyr	Thr	Lys	Gln	Lys	Tyr	Pro	Glu	Gln	Pro	Gly	Arg	Phe	Ala	Lys	
		405				410					415					
ctg	ctg	ctg	cgc	ctc	cca	gct	ctg	cgt	tcc	att	ggc	ttg	aaa	tgc	ctg	1593
Leu	Leu	Leu	Arg	Leu	Pro	Ala	Leu	Arg	Ser	Ile	Gly	Leu	Lys	Cys	Leu	
	420					425					430					

gag cac ctc ttc ttc ttc aag ctc atc ggg gac acc ccc att gac acc 1641  
 Glu His Leu Phe Phe Phe Lys Leu Ile Gly Asp Thr Pro Ile Asp Thr  
 435 440 445 450

ttc ctc atg gag atg ttg gag acc ccg ctg cag atc acc tga 1683  
 Phe Leu Met Glu Met Leu Glu Thr Pro Leu Gln Ile Thr \*  
 455 460

gccccaccag ccacagcctc cccacccagg atgacccttg ggcaggtgtg tgtggacccc 1743  
 caccctgcac tttcctccac ctcccaccct gaccccttc ctgtccccaa aatgtgatgc 1803  
 ttataataaaa gaaaaccttt ctac 1827

<210> 16  
 <211> 463  
 <212> PRT  
 <213> Homo Sapien

<400> 16  
 Met Tyr Gly Asn Tyr Ser His Phe Met Lys Phe Pro Ala Gly Tyr Gly  
 1 5 10 15  
 Gly Ser Pro Gly His Thr Gly Ser Thr Ser Met Ser Pro Ser Ala Ala  
 20 25 30  
 Leu Ser Thr Gly Lys Pro Met Asp Ser His Pro Ser Tyr Thr Asp Thr  
 35 40 45  
 Pro Val Ser Ala Pro Arg Thr Leu Ser Ala Val Gly Thr Pro Leu Asn  
 50 55 60  
 Ala Leu Gly Ser Pro Tyr Arg Val Ile Thr Ser Ala Met Gly Pro Pro  
 65 70 75 80  
 Ser Gly Ala Leu Ala Pro Pro Gly Ile Asn Leu Val Ala Pro Pro  
 85 90 95  
 Ser Ser Gln Leu Asn Val Val Asn Ser Val Ser Ser Ser Glu Asp Ile  
 100 105 110  
 Lys Pro Leu Pro Gly Leu Pro Gly Ile Gly Asn Met Asn Tyr Pro Ser  
 115 120 125  
 Thr Ser Pro Gly Ser Leu Val Lys His Ile Cys Ala Ile Cys Gly Asp  
 130 135 140  
 Arg Ser Ser Gly Lys His Tyr Gly Val Tyr Ser Cys Glu Gly Cys Lys  
 145 150 155 160  
 Gly Phe Phe Lys Arg Thr Ile Arg Lys Asp Leu Ile Tyr Thr Cys Arg  
 165 170 175  
 Asp Asn Lys Asp Cys Leu Ile Asp Lys Arg Gln Arg Asn Arg Cys Gln  
 180 185 190  
 Tyr Cys Arg Tyr Gln Lys Cys Leu Val Met Gly Met Lys Arg Glu Ala  
 195 200 205  
 Val Gln Glu Glu Arg Gln Arg Ser Arg Glu Arg Ala Glu Ser Glu Ala  
 210 215 220  
 Glu Cys Ala Thr Ser Gly His Glu Asp Met Pro Val Glu Arg Ile Leu  
 225 230 235 240  
 Glu Ala Glu Leu Ala Val Glu Pro Lys Thr Glu Ser Tyr Gly Asp Met  
 245 250 255  
 Asn Met Glu Asn Ser Thr Asn Asp Pro Val Thr Asn Ile Cys His Ala  
 260 265 270  
 Ala Asp Lys Gln Leu Phe Thr Leu Val Glu Trp Ala Lys Arg Ile Pro  
 275 280 285  
 His Phe Ser Asp Leu Thr Leu Glu Asp Gln Val Ile Leu Leu Arg Ala  
 290 295 300  
 Gly Trp Asn Glu Leu Leu Ile Ala Ser Phe Ser His Arg Ser Val Ser  
 305 310 315 320  
 Val Gln Asp Gly Ile Leu Leu Ala Thr Gly Leu His Val His Arg Ser  
 325 330 335  
 Ser Ala His Ser Ala Gly Val Gly Ser Ile Phe Asp Arg Val Leu Thr  
 340 345 350  
 Glu Leu Val Ser Lys Met Lys Asp Met Gln Met Asp Lys Ser Glu Leu  
 355 360 365  
 Gly Cys Leu Arg Ala Ile Val Leu Phe Asn Pro Asp Ala Lys Gly Leu  
 370 375 380  
 Ser Asn Pro Ser Glu Val Glu Thr Leu Arg Glu Lys Val Tyr Ala Thr



Gly	Asp	Gly	Glu	Gly	Ala	Gly	Gly	Ala	Pro	Glu	Glu	Met	Pro	Val	Asp	
				155					160					165		
agg	atc	ctg	gag	gca	gag	ctt	gct	gtg	gaa	cag	aag	agt	gac	cag	ggc	642
Arg	Ile	Leu	Glu	Ala	Glu	Leu	Ala	Val	Glu	Gln	Lys	Ser	Asp	Gln	Gly	
			170					175					180			
gtt	gag	ggg	cct	ggg	gga	acc	ggg	ggg	agc	ggc	agc	agc	gtg	agt	gtt	690
Val	Glu	Gly	Pro	Gly	Gly	Thr	Gly	Gly	Ser	Gly	Ser	Ser	Val	Ser	Val	
		185					190					195				
ggg	gtc	aat	cca	ctc	tcc	ttc	gtg	atg	ggg	gtt	ggg	gga	ggc	agt	cta	738
Gly	Val	Asn	Pro	Leu	Ser	Phe	Val	Met	Gly	Val	Gly	Gly	Gly	Ser	Leu	
	200					205					210					
ggg	ctg	ttc	tac	atc	ccc	tcc	ccc	tcc	ttt	ccc	ctc	ata	acc	ttc	cta	786
Gly	Leu	Phe	Tyr	Ile	Pro	Ser	Pro	Ser	Phe	Pro	Leu	Ile	Thr	Phe	Leu	
	215				220				225						230	
aca	cta	ctt	ggg	act	gga	ggg	gct	gcc	aaa	caa	ggg	ctt	tca	aac	atc	834
Thr	Leu	Leu	Gly	Thr	Gly	Gly	Ala	Ala	Lys	Gln	Gly	Leu	Ser	Asn	Ile	
				235					240					245		
tga	ggg	gat	gtg	atag	ctc	ctt	ctgt	ctc	ac	cccc	aa	aca	acc	ctg	ggc	887
*																

aga	acc	atag	gcat	gtcc	ca	aata	aaata	at	tg	ttt	gc	act	aat	gcc	agaa	gaga	agact	947	
act	tac	aggg	att	gg	ttt	gg	at	ggg	gct	ca	cag	ga	act	atat	gta	agg	agggg	gtg	1007
aaa	agc	ctct	taca	aggg	ggg	ctcc	ag	cat	atct	caaa	at	ctt	ccata	ac	tctt	acccc		1067	
gtc	ccct	gca	gcca	aat	gac	cct	gt	gacta	acat	ct	gt	ca	ggc	ag	ct	gac	aaac	agct	1127
tcac	gct	ttg	tgag	tggg	cgc	aag	agg	atcc	cac	act	ttt	ctc	ctt	gc	ct	tg	gat	gat	1187
agg	tcat	att	gct	gc	ggg	gca	gg	tcag	tgac	ctt	gg	atccc	ttt	gac	ttct	tgac	attt	ga	1247
ccc	ctct	ttt	act	tccc	gat	cttt	agt	tgac	ccc	ag	tgg	gcc	ttac	ctt	g	tacc	cagg	ga	1307
gcca	aact	tg	ctg	ac	ctgc	cac													1330

<210> 18  
 <211> 246  
 <212> PRT  
 <213> Homo Sapien

<400>	18																		
Met	Ile	Ser	Ile	Thr	Ser	Val	Thr	Phe	Cys	Phe	Pro	Ile	Ser	Leu	Pro				
1				5					10					15					
Val	Thr	Ser	Leu	Phe	Pro	Pro	Ser	Gln	Ile	Asn	Ser	Thr	Val	Ser	Leu				
			20					25					30						
Pro	Gly	Gly	Gly	Ser	Gly	Pro	Pro	Glu	Asp	Val	Lys	Pro	Pro	Val	Leu				
		35					40					45							
Gly	Val	Arg	Gly	Leu	His	Cys	Pro	Pro	Pro	Pro	Gly	Gly	Pro	Gly	Ala				
	50					55					60								
Gly	Lys	Arg	Leu	Cys	Ala	Ile	Cys	Gly	Asp	Arg	Ser	Ser	Gly	Lys	His				
	65				70				75					80					
Tyr	Gly	Val	Tyr	Ser	Cys	Glu	Gly	Cys	Lys	Gly	Phe	Phe	Lys	Arg	Thr				
			85					90						95					
Ile	Arg	Lys	Asp	Leu	Thr	Tyr	Ser	Cys	Arg	Asp	Asn	Lys	Asp	Cys	Thr				
			100					105					110						
Val	Asp	Lys	Arg	Gln	Arg	Asn	Arg	Cys	Gln	Tyr	Cys	Arg	Tyr	Gln	Lys				
		115					120						125						
Cys	Leu	Ala	Thr	Gly	Met	Lys	Arg	Glu	Ala	Val	Gln	Glu	Glu	Arg	Gln				
	130					135					140								
Arg	Gly	Lys	Asp	Lys	Asp	Gly	Asp	Gly	Glu	Gly	Ala	Gly	Gly	Ala	Pro				
	145				150				155					160					
Glu	Glu	Met	Pro	Val	Asp	Arg	Ile	Leu	Glu	Ala	Glu	Leu	Ala	Val	Glu				
				165				170						175					
Gln	Lys	Ser	Asp	Gln	Gly	Val	Glu	Gly	Pro	Gly	Gly	Thr	Gly	Gly	Ser				
			180					185					190						
Gly	Ser	Ser	Val	Ser	Val	Gly	Val	Asn	Pro	Leu	Ser	Phe	Val	Met	Gly				

		195					200					205					
Val	Gly	Gly	Gly	Ser	Leu	Gly	Leu	Phe	Tyr	Ile	Pro	Ser	Pro	Ser	Phe		
	210					215					220						
Pro	Leu	Ile	Thr	Phe	Leu	Thr	Leu	Leu	Gly	Thr	Gly	Gly	Ala	Ala	Lys		
225					230					235					240		
Gln	Gly	Leu	Ser	Asn	Ile												
				245													